GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2005, 03:02:43 ; Search time 75.3571 Seconds
                                                     (without alignments)
                                                     29.153 Million cell updates/sec

Title: US-10-805-881-1
Perfect Score: 27
Sequence: 1 FFGLM 5
Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 990051

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_21:*
               1: geneseqp1980s:*
               2: geneseqp1990s:*
               3: geneseqp2000s:*
               4: geneseqp2001s:*
               5: geneseqp2002s:*
               6: geneseqp2003as:*
               7: geneseqp2003bs:*
               8: geneseqp2004s:*
               9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	27	100.0	5	2	AAR33009	Aar33009 Alpha-sub
2	27	100.0	5	2	AAR33008	Aar33008 Alpha-sub
3	27	100.0	5	2	AAR33007	Aar33007 Alpha-sub
4	27	100.0	5	2	AAR33010	Aar33010 Alpha-sub
5	27	100.0	5	2	AAR54549	Aar54549 Cholecyst
6	27	100.0	5	2	AAR54551	Aar54551 Cholecyst
7	27	100.0	5	2	AAR54550	Aar54550 Cholecyst
8	27	100.0	5	2	AAR54548	Aar54548 Cholecyst
9	27	100.0	5	2	AAW41687	Aaw41687 Tetrapept
10	27	100.0	5	2	AAW99643	Aaw99643 Substance
11	27	100.0	5	2	AAY50325	Aay50325 Neutrophi
12	27	100.0	5	2	AAW92660	Aaw92660 Human tac
13	27	100.0	5	3	AAB23025	Aab23025 Human/rat
14	27	100.0	5	3	AAY67576	Aay67576 P antagon
15	27	100.0	5	4	AAB91428	Aab91428 Tachykini
16	27	100.0	5	5	ABB10088	Abb10088 Substance
17	27	100.0	5	5	AAU77845	Aau77845 Tachykini
18	27	100.0	5	7	ADE94203	Ade94203 High acti
19	27	100.0	5	7	ADF92530	Adf92530 Substance
20	27	100.0	5	8	ADN95078	Adn95078 Mammalian
21	27	100.0	5	9	ADR43771	Adr43771 Human mag
22	27	100.0	5	9	ADV44808	Adv44808 Mammalian
23	27	100.0	6	1	AAP40519	Aap40519 Sequence
24	27	100.0	6	1	AAP50694	Aap50694 Sequence
25	27	100.0	6	1	AAP50632	Aap50632 Substance
26	27	100.0	6	1	AAP61486	Aap61486 Peptide h
27	27	100.0	6	2	AAR07893	Aar07893 Cyclopept
28	27	100.0	6	2	AAR21959	Aar21959 Substance
29	27	100.0	6	2	AAR27694	Aar27694 Cyclic ta
30	27	100.0	6	2	AAW99686	Aaw99686 Substance
31	27	100.0	6	2	AAW92706	Aaw92706 Human tac
32	27	100.0	6	2	AAW92659	Aaw92659 Human tac
33	27	100.0	6	3	AAY67575	Aay67575 P antagon
34	27	100.0	6	4	AAB82453	Aab82453 Fluorinat
35	27	100.0	6	4	AAB82436	Aab82436 Fluorinat
36	27	100.0	6	4	AAB91425	Aab91425 Tachykini
37	27	100.0	6	4	AAB91421	Aab91421 Tachykini
38	27	100.0	6	4	AAB91419	Aab91419 Atypical
39	27	100.0	6	4	AAG99351	Aag99351 Atypical
40	27	100.0	6	4	AAB98884	Aab98884 Chimeric
41	27	100.0	6	4	AAB98886	Aab98886 Chimeric
42	27	100.0	6	5	ABB10086	Abb10086 Substance
43	27	100.0	6	7	ADE94202	Ade94202 High acti
44	27	100.0	7	2	AAR21956	Aar21956 Substance
45	27	100.0	7	2	AAR21957	Aar21957 Substance

ALIGNMENTS

RESULT 1
AAR33009
ID   AAR33009 standard; peptide; 5 AA.
XX
AC   AAR33009;
XX
DT   25-MAR-2003 (revised)
DT   02-APR-1993 (first entry)
XX
DE   Alpha-substituted short peptide.
XX
KW   CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
KW   improved bioavailability.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   Modified-site   4
FT   /note= "alpha-Me-Leu"
FT   Modified-site   5
FT   /note= "Met-NH2"
XX
PN   WO9219254-A1.
XX
PD   12-NOV-1992.
XX
PF   15-APR-1992; 92WO-US003119.
XX
PR   24-APR-1991; 91US-00690755.
PR   20-MAR-1992; 92US-00852086.
XX
PA   (WARN) WARNER LAMBERT CO.
XX
PI   Horwell DC, Hughes J, Richardson RS, Howson W;
XX
DR   WPI; 1992-398522/48.
XX
PT   New alpha-substd. polypeptide are e.g. selective receptor ligands - for
PT   treating inflammation, pain, stroke, ulcers, hypertension, heart failure,
PT   depression, cancer, asthma, psychosis, arthritis, etc.
XX
PS   Claim 3; Page 41; 46pp; English.
XX
CC   The peptide is a specifically claimed example of a group of generically
CC   claimed mono-, di-, tri-, tetra- and penta-peptides which include a
CC   substituent on an alpha-C atom in the chain. Such substitution may modify
CC   the bioavailability, stability or absorbability of the peptide and hence

(RESULT 1 — continued)

```
CC   may improve the activity of the peptide as a drug. Depending on the
CC   nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic
CC   peptide, etc.), the modified peptides are variously useful for treating
CC   obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,
CC   addictive drug withdrawal symptoms, hypertension, heart failure,
CC   cognition or memory disorders, spasticity, depression, diabetes, cancer,
CC   asthma, bladder dysfunction, psychosis and arthritis; and as
CC   contraceptives. (Updated on 25-MAR-2003 to correct PD field.) (Updated on
CC   25-MAR-2003 to correct PI field.) (Updated on 25-MAR-2003 to correct PR
XX   field.) (Updated on 25-MAR-2003 to correct PN field.)
SQ   Sequence 5 AA;
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Qy    1 FFGLM 5
        |||||
Db    1 FFGLM 5
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Query Match        100.0%;   Score 27;  DB 2;   Length 5;
Best Local Similarity   100.0%;   Pred. No. 2e+06;
Matches   5;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
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RESULT 2
AAR33008
ID   AAR33008 standard; peptide; 5 AA.
AC   AAR33008;
XX
DT   25-MAR-2003  (revised)
DT   02-APR-1993  (first entry)
XX
DE   Alpha-substituted short peptide.
XX
KW   CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
KW   improved bioavailability.
XX
OS   Synthetic.
XX
FH   Key           Location/Qualifiers
FT   Modified-site 2
FT                 /note= "alpha-Me-Phe"
FT   Modified-site 5
FT                 /note= "Met-NH2"
XX
PN   WO9219254-A1.
XX
PD   12-NOV-1992.
XX
PF   15-APR-1992;  92WO-US003119.
XX
PR   24-APR-1991;  91US-0069075S.
PR   20-MAR-1992;  92US-0085208G.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Horwell DC, Hughes J, Richardson RS, Howson W;
XX
DR   WPI; 1992-398522/48.
XX
PT   New alpha-substd. polypeptide are e.g. selective receptor ligands - for
PT   treating inflammation, pain, stroke, ulcers, hypertension, heart failure,
PT   depression, cancer, asthma, psychosis, arthritis, etc.
XX
PS   Claim 3; Page 41; 46pp; English.
XX
CC   The peptide is a specifically claimed example of a group of generically
CC   claimed mono-, di-, tri-, tetra- and penta-peptides which include a
CC   substituent on an alpha-C atom in the chain. Such substitution may modify
CC   the bioavailability, stability or absorbability of the peptide and hence
CC   may improve the activity of the peptide as a drug. Depending on the
CC   nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic
CC   peptide, etc.), the modified peptides are variously useful for treating
CC   obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,
```

```
CC   addictive drug withdrawal symptoms, hypertension, heart failure,
CC   cognition or memory disorders, spasticity, depression, diabetes, cancer,
CC   asthma, bladder dysfunction, psychosis and arthritis; and as
CC   contraceptives. (Updated on 25-MAR-2003 to correct PD field.) (Updated on
CC   25-MAR-2003 to correct PI field.) (Updated on 25-MAR-2003 to correct PR
CC   field.) (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 5 AA;
```

```
Qy    1 FFGLM 5
        |||||
Db    1 FFGLM 5
```

```
Query Match        100.0%;   Score 27;  DB 2;   Length 5;
Best Local Similarity   100.0%;   Pred. No. 2e+06;
Matches   5;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
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```
RESULT 3
AAR33007
ID   AAR33007 standard; peptide; 5 AA.
AC   AAR33007;
XX
DT   25-MAR-2003  (revised)
DT   02-APR-1993  (first entry)
XX
DE   Alpha-substituted short peptide.
XX
KW   CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
KW   improved bioavailability.
XX
OS   Synthetic.
XX
FH   Key           Location/Qualifiers
FT   Modified-site 1
FT                 /note= "alpha-Me-Phe"
FT   Modified-site 5
FT                 /note= "Met-NH2"
XX
PN   WO9219254-A1.
XX
PD   12-NOV-1992.
XX
PF   15-APR-1992;  92WO-US003119.
XX
PR   24-APR-1991;  91US-00690755.
PR   20-MAR-1992;  92US-0085208G.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Horwell DC, Hughes J, Richardson RS, Howson W;
XX
DR   WPI; 1992-398522/48.
XX
PT   New alpha-substd. polypeptide are e.g. selective receptor ligands - for
PT   treating inflammation, pain, stroke, ulcers, hypertension, heart failure,
PT   depression, cancer, asthma, psychosis, arthritis, etc.
XX
PS   Claim 3; Page 41; 46pp; English.
XX
CC   The peptide is a specifically claimed example of a group of generically
CC   claimed mono-, di-, tri-, tetra- and penta-peptides which include a
CC   substituent on an alpha-C atom in the chain. Such substitution may modify
CC   the bioavailability, stability or absorbability of the peptide and hence
CC   may improve the activity of the peptide as a drug. Depending on the
CC   nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic
CC   peptide, etc.), the modified peptides are variously useful for treating
CC   obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,
CC   addictive drug withdrawal symptoms, hypertension, heart failure,
CC   cognition or memory disorders, spasticity, depression, diabetes, cancer,
CC   asthma, bladder dysfunction, psychosis and arthritis; and as
CC   contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on
```

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: November 26, 2005, 03:18:04 ; Search time 20 Seconds
(without alignments)
24.054 Million cell updates/sec

Title: US-10-805-881-1
Perfect score: 27
Sequence: 1 FFGLM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 6283

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	27	100.0	11	1	A60654	substance P - guin
2	27	100.0	11	2	SPHO	substance P - hors
3	27	100.0	11	2	JN0023	substance P - chic
4	27	100.0	11	2	S33300	probable substance
5	27	100.0	11	2	E60409	substance P-like p
6	27	100.0	11	2	F60409	substance P-like p
7	27	100.0	11	2	S23308	substance P - rain
8	24	88.9	10	2	B49581	substance P - rain
9	24	88.9	10	2	B61033	ranatachykinin B -
10	24	88.9	10	2	A49581	ranatachykinin B - yel
11	24	88.9	10	2	A49581	sialokinin I - s
12	24	88.9	10	2	S07203	scyliorhinin I - s
13	24	88.9	11	2	S07201	uperolein - frog (
14	24	88.9	11	2	A61033	physalaemin - frog
15	22	81.5	12	2	S07436	ranatachykinin A -
16	22	81.5	28	2	T06925	tachykinin - Afric
17	21	77.8	10	2	S07202	hypothetical prote
18	21	77.8	10	2	C61033	phyllomedulin - tw
19	21	77.8	10	2	S27178	neurokinin A-relat
20	21	77.8	11	1	E0OC	tachykinin C -
21	21	77.8	11	1	EOCC	eledoisin - musky
22	21	77.8	11	2	S23306	substance P - Atla
23	21	77.8	19	2	PS0332	phospholipase A2 (
24	21	77.8	24	1	S15649	H+-transporting tw
25	20	74.1	10	1	SPPGNK	neuromedin K - pig
26	20	74.1	10	2	JN0024	neuromedin K - pig
27	20	74.1	10	2	S23307	neurokinin A - chi
28	20	74.1	10	2	S23186	neurokinin A - rai
29	20	74.1	11	2	C60409	kassinin-like pept
30	20	74.1	11	2	B60409	kassinin-like pept
31	20	74.1	11	2	D60409	kassinin-like pept
32	20	74.1	12	2	S10059	tachykinin - Afric
33	20	74.1	12	2	S07206	kassinin - Senegal
34	20	74.1	16	2	A60839	neurokinin A homol
35	20	74.1	18	2	B24867	scyliorhinin II -
36	20	74.1	21	2	JH0361	carassin - goldfis
37	19	70.4	18	2	S74144	aggrecan - bovine
38	19	70.4	18	2	I52651	brain-derived neur
39	19	70.4	5	2	PT0278	Ig heavy chain CRD
40	18	66.7	10	2	PT0807	T-cell receptor al
41	18	66.7	12	2	PH0807	T-cell receptor be
42	18	66.7	12	2	S26554	T-cell receptor be
43	18	66.7	12	2	S26559	T-cell receptor be
44	18	66.7	12	2	S26555	T-cell receptor be
45	18	66.7	12	2	PH1467	T-cell receptor be

ALIGNMENTS

RESULT 1
A60654
substance P - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: A60654
R;Murphy, R.
Neuropeptides 14, 105-110, 1989
A;Title: Primary amino acid sequence of guinea-pig substance P.
A;Reference number: A60654; MUID:90044685; PMID:2478925
A;Accession: A60654
A;Molecule type: protein
A;Residues: 1-11 <MUR>
A;Cross-references: UNIPROT:P01290; UNIPARC:UPI000002BD74
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match　　　100.0%;　Score 27;　DB 1;　Length 11;
Best Local Similarity　100.0%;　Pred. No. 2.9;
Matches　5;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

Qy　　1 FFGLM 5
　　　　　|||||
Db　　7 FFGLM 11

RESULT 2
SPHO
substance P - horse
C;Species: Equus caballus (domestic horse)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C;Accession: A01558
R;Studer, R.O.; Trzeciak, A.; Lergier, W.
Helv. Chim. Acta 56, 860-866, 1973
A;Title: Isolierung und Aminosäuresequenz von Substanz P aus Pferdedarm.
A;Reference number: A01558
A;Accession: A01558
A;Molecule type: protein
A;Residues: 1-11 <STU>
A;Cross-references: UNIPROT:P01290; UNIPARC:UPI000002BD74
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; hormone
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match　　　100.0%;　Score 27;　DB 1;　Length 11;
Best Local Similarity　100.0%;　Pred. No. 2.9;
Matches　5;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

Qy　　1 FFGLM 5
　　　　　|||||
Db　　7 FFGLM 11

RESULT 3
JN0023
substance P - chicken
C;Species: Gallus gallus (chicken)
A;Accession: JN0023
A;Molecule type: protein
A;Residues: 1-11 <CON>
A;Cross-references: UNIPROT:P19850; UNIPARC:UPI000003524J
A;Reference number: JN0023; MUID:88204263; PMID:2452461
A;Title: [Arg3]substance P and neurokinin A from chicken small intestine.
Regul. Pept. 20, 171-180, 1988
A;Reference number: JN0023
R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
A;Superfamily: substance P precursor
A;Keywords: amidated carboxyl end; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

```
Qy   1 FFGLM 5
       |||||
Db   7 FFGLM 11
```

Query Match   100.0%; Score 27; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 4
S33300
probable substance P - smaller spotted catshark
C;Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
A;Accession: S33300
A;Molecule type: protein
A;Residues: 1-11 <WAU>
A;Cross-references: UNIPROT:P41333; UNIPARC:UPI000013FDB
A;Experimental source: brain
A;Function:
A;Description: may play a physiological role in the regulation of cardiovascular and gas
A;Note: substance P is derived by post-translational processing of preprotachykinin A
R;Waugh, D.; Wang, Y.; Hazon, N.; Balment, R.J.; Conlon, J.M.
Eur. J. Biochem. 214, 469-474, 1993
A;Title: Primary structures and biological activities of substance-P-related peptides fr
A;Reference number: S33300; MUID:93292508; PMID:7685693
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
A;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

```
Qy   1 FFGLM 5
       |||||
Db   7 FFGLM 11
```

Query Match   100.0%; Score 27; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 5
E60409
substance P-like peptide I - frog (Pseudophryne guntheri)
C;Species: Pseudophryne guntheri
A;Accession: E60409
A;Molecule type: protein
A;Residues: 1-11 <SIM>
A;Cross-references: UNIPROT:P42989; UNIPARC:UPI000136FD8
A;Reference number: A60409; MUID:90287814; PMID:2356157
A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austra
R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 16-Aug-2004
C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

```
Qy   1 FFGLM 5
       |||||
Db   7 FFGLM 11
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Query Match   100.0%; Score 27; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 6
F60409
substance P-like peptide II - frog (Pseudophryne guntheri)
C;Species: Pseudophryne guntheri
C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 16-Aug-2004
C;Accession: F60409
R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austra
A;Reference number: A60409; MUID:90287814; PMID:2356157
A;Accession: F60409
A;Molecule type: protein
A;Residues: 1-11 <SIM>
A;Cross-references: UNIPROT:P42990; UNIPARC:UPI000136FD9
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

```
Qy   1 FFGLM 5
       |||||
Db   7 FFGLM 11
```

Query Match   100.0%; Score 27; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 7
S23308
substance P - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
C;Accession: S23308
R;Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod
A;Reference number: S23186; MUID:92298992; PMID:1376687
A;Accession: S23308
A;Molecule type: protein
A;Residues: 1-11 <JEN>
A;Cross-references: UNIPROT:P28499; UNIPARC:UPI000003525A
A;Description: may play a physiological role in the regulation of cardiovascular and gas
A;Function:
A;Experimental source: brain
A;Note: substance P is derived by post-translational processing of preprotachykinin A
A;Keywords: neuropeptide; amidated carboxyl end; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

```
Qy   1 FFGLM 5
       |||||
Db   7 FFGLM 11
```

Query Match   100.0%; Score 27; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 8
B49581
sialokinin II - yellow fever mosquito

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: November 26, 2005, 03:17:04 ; Search time 122.5 Seconds
(without alignments)
28.797 Million cell updates/sec

Title: US-10-805-881-1
Perfect score: 27
Sequence: 1 FFGLM 5

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 34439

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : UniProt_05.80:*
         1: uniprot_sprot:*
         2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	27	100.0	11	1	P42989 TKN4_PSEGU	pseudophryn
2	27	100.0	11	1	P42990 TKN5_PSEGU	pseudophryn
3	27	100.0	11	1	P67932 TKNA_CAVPO	cavia porce
4	27	100.0	11	1	P19850 TKNA_CHICK	gallus gall
5	27	100.0	11	1	P67933 TKNA_HORSE	equus cabal
6	27	100.0	11	1	P28499 TKNA_ONCMY	oncorhynchu
7	27	100.0	11	1	P41333 TKNA_SCYCA	scyliorhinu
8	27	88.9	10	1	P08608 TKN1_SCYCA	scyliorhinu
9	24	88.9	10	1	P22689 TKNB_RANCA	rana catesb
10	24	88.9	10	1	P42634 TKS1_AEDAE	aedes aegyp
11	24	88.9	10	1	P42635 TKS2_AEDAE	aedes aegyp
12	24	88.9	11	1	P82026 TKN1_UPEIN	uperoleia i
13	24	88.9	11	1	P08608 TKN1_UPERU	uperoleia r
14	24	88.9	11	1	P08612 TKN2_UPERU	uperoleia r
15	24	88.9	11	1	P08616 TKN1_UPERU	uperoleia r
16	24	88.9	11	1	P29207 TKNA_RANRI	rana ridibu
17	24	88.9	11	1	P28615 TKN_PHYFU	physalaemus
18	24	88.9	11	1	P09951 TKN_PHYFU	physalaemus
19	24	88.9	14	1	P80951 TKNM_RANMA	rana margar
20	24	88.9	25	2	Q80VX3_MOUSE	mus musculu
21	24	88.9	26	2	Q4TDF2_TETNG	tetraodon n
22	23	85.2	30	2	Q5N289_SYNP6	synechococc
23	22	81.5	12	1	P08614 TKN2_KASMA	kassina mac
24	22	81.5	25	2	Q8KIT2_MOUSE	mus musculu
25	22	81.5	27	2	Q8KIT2_MOUSE	mus musculu
26	22	81.5	28	1	P48102 PETL_CYAPA	cyanophora
27	22	81.5	28	2	Q4YTJ2_PLABE	plasmodium
28	22	77.8	10	1	P29135 TKNB_RANRI	rana ridibu
29	21	77.8	10	1	P22690 TKNC_RANCA	rana catesb
30	21	77.8	10	1	P08610 TKN_PHYBI	phyllomedus
31	21	77.8	11	2	Q76ML8_9TELE	eurypharynx
32	21	77.8	11	1	P28498 TKNA_GADMO	gadus morhu
33	21	77.8	11	1	P62933 TKN_ELECI	eledone cir
34	21	77.8	11	1	P62934 TKN_ELEMO	eledone mos
35	21	77.8	19	1	P24606 PA25_HUMAN	homo sapien
36	21	77.8	23	2	Q9S8E2_SPIOL	spinacia ol
37	21	77.8	23	2	Q99221_MELJA	meloidogyne
38	21	77.8	27	2	Q4xbu6_PLACH	plasmodium
39	21	77.8	29	2	Q4SBA4_TETNG	tetraodon n
40	21	74.1	10	2	Q673E3_9CHLR	dehalococco
41	21	74.1	10	1	P69144 TKNB_CHICK	gallus gall
42	21	74.1	10	1	P19851 TKNB_GADMO	gadus morhu
43	21	74.1	10	1	P69143 TKNB_ONCMY	oncorhynchu
44	21	74.1	10	1	P67934 TKNK_RANRI	rana ridibu
44	21	74.1	10	1	P67935 TKNK_RANRI	rana ridibu
45	21	74.1	10	1	P81738 TRP6_LEUMA	leucophaea

ALIGNMENTS

RESULT 1
TKN4_PSEGU

ID   TKN4_PSEGU   STANDARD;   PRT;   11 AA.
AC   P42989;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Substance P-like peptide I (PG-SPI).
OS   Pseudophryne guentheri (Guenther's toadlet).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC   Myobatrachinae; Pseudophryne.
OX   NCBI_TaxID=30349;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Skin secretion;
RX   MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;
RA   Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA   Roberts J.D., Melchiorri P., Erspamer V.;
RT   "Six novel tachykinin- and bombesin-related peptides from the skin of
RT   the Australian frog Pseudophryne guntheri.";
RL   Peptides 11:299-304(1990).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC   evoke behavioral responses, are potent vasodilators and
CC   secretagogues, and contract (directly or indirectly) many smooth
CC   muscles.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed by the skin glands.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   PIR; E60409; E60409.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   InterPro; IPR008215; TachyKinin.
DR   Pfam; PF02202; Tachykinin; 1.
DR   SMART; SM00203; TK; 1.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Amidation; Amphibian defense peptide; Direct protein sequencing;
KW   Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.
FT   MOD_RES   1   1   Pyrrolidone carboxylic acid.
FT   MOD_RES   11   11   Methionine amide.
SQ   SEQUENCE   11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match   100.0%; Score 27; DB 1; Length 11;
Best Local Similarity   100.0%;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FFGLM 5
              |||||
Db   1 FFGLM 5

Db   7 FFGLM 11

RESULT 2
ID   TKN5_PSEGU   STANDARD;   PRT;   11 AA.
AC   P42290;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Substance P-like peptide II (PG-SPII).
OS   Pseudophryne guentheri (Guenther's toadlet).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC   Myobatrachinae; Pseudophryne.
OX   NCBI_TaxID=30349;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Skin secretion;
RX   MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;
RA   Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA   Roberts J.D., Melchiorri P., Erspamer V.;
RT   "Six novel tachykinin- and bombesin-related peptides from the skin of
RT   the Australian frog Pseudophryne guentheri.";
RL   Peptides 11:299-304(1990).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC   evoke behavioral responses, are potent vasodilators and
CC   secretagogues, and contract (directly or indirectly) many smooth
CC   muscles.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed by the skin glands.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
CC   ---
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---
DR   PIR; F60409; F60409.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   Pfam; PF02202; Tachykinin; 1.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Amidation; Amphibian defense peptide; Direct protein sequencing;
KW   Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.
FT   MOD_RES   1   1   Pyrrolidone carboxylic acid.
FT   MOD_RES   11   11   Methionine amide.
SQ   SEQUENCE   11 AA;   1293 MW; 3A247C2CC9CB1457 CRC64;

Query Match   100.0%;   Score 27;   DB 1;   Length 11;
Best Local Similarity   100.0%;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FFGLM 5
         |||||
Db   7 FFGLM 11

RESULT 3
ID   TKNA_CAVPO   STANDARD;   PRT;   11 AA.
AC   P67932; P01290;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Substance P.
GN   Name=TAC1; Synonyms=NKA, NKNA, TAC2;
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC   Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Small intestine;
RX   MEDLINE=90044685; PubMed=2478925; DOI=10.1016/0143-4179(89)90066-8;
RA   Murphy R.;
RT   "Primary amino acid sequence of guinea-pig substance P.";
RL   Neuropeptides 14:105-110(1989).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC   evoke behavioral responses, are potent vasodilators and
CC   secretagogues, and contract (directly or indirectly) many smooth
CC   muscles.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
CC   ---
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---
DR   PIR; A60654; A60654.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   Pfam; PF02202; Tachykinin; 1.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Amidation; Direct protein sequencing; Neuropeptide; Neurotransmitter;
KW   Tachykinin.
FT   MOD_RES   11   11   Methionine amide.
SQ   SEQUENCE   11 AA;   1349 MW; 3B757FB3C9D6C6C7 CRC64;

Query Match   100.0%;   Score 27;   DB 1;   Length 11;
Best Local Similarity   100.0%;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FFGLM 5
         |||||
Db   7 FFGLM 11

RESULT 4
ID   TKNA_CHICK   STANDARD;   PRT;   11 AA.
AC   P19850;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Substance P.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Intestine;
RX   MEDLINE=88204263; PubMed=2452461; DOI=10.1016/0167-0115(88)90050-X;
RA   Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
RT   "[Arg3]substance P and neurokinin A from chicken small intestine.";
RL   Regul. Pept. 20:171-180(1988).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC   evoke behavioral responses, are potent vasodilators and
CC   secretagogues, and contract (directly or indirectly) many smooth
CC   muscles.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
CC   ---
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---
DR   PIR; JN0023; JN0023.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   Pfam; PF02202; Tachykinin; 1.

Qy   1 FFGLM 5
         |||||
Db   7 FFGLM 11

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: November 26, 2005, 03:06:43 ; Search time 20 Seconds
                                    (without alignments)
                                    20.669 Million cell updates/sec

Title: US-10-805-881-1
Perfect score: 27
Sequence: 1 FFGLM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 265581

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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    3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
    4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
    5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
    6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% Match	Length	DB	ID	Description
1	27	100.0	5	5	1	US-07-934-553-2	Sequence 2, Appli
2	27	100.0	5	5	1	US-08-225-474-2	Sequence 2, Appli
3	27	100.0	5	5	1	US-07-737-371E-6	Sequence 6, Appli
4	27	100.0	5	5	2	US-09-265-690C-1	Sequence 1, Appli
5	27	100.0	5	5	2	US-09-623-548A-604	Sequence 604, App
6	27	100.0	5	5	2	US-10-134-187-3	Sequence 3, Appli
7	27	100.0	5	5	2	US-09-657-276-604	Sequence 604, App
8	27	100.0	5	5	1	US-07-934-553-3	Sequence 3, Appli
9	27	100.0	6	1	1	US-08-225-474-3	Sequence 3, Appli
10	27	100.0	6	1	1	US-08-430-238-15	Sequence 15, Appli
11	27	100.0	6	1	1	US-07-737-371E-5	Sequence 5, Appli
12	27	100.0	6	1	1	US-09-317-125-5	Sequence 5, Appli
13	27	100.0	6	2	1	US-09-428-692-39	Sequence 39, Appli
14	27	100.0	6	2	1	US-09-428-692-41	Sequence 41, Appli
15	27	100.0	6	2	2	US-09-623-548A-595	Sequence 595, App
16	27	100.0	6	2	2	US-09-623-548A-597	Sequence 597, App
17	27	100.0	6	2	2	US-09-657-276-595	Sequence 595, App
18	27	100.0	6	2	2	US-09-657-276-597	Sequence 597, App
19	27	100.0	6	2	2	US-09-623-548A-601	Sequence 601, App
20	27	100.0	6	2	2	US-09-657-276-601	Sequence 601, App
21	27	100.0	7	1	1	US-07-712-828B-7	Sequence 7, Appli
22	27	100.0	7	2	1	US-07-737-371E-8	Sequence 8, Appli
23	27	100.0	7	2	1	US-09-428-692-42	Sequence 42, Appli
24	27	100.0	7	2	2	US-09-623-548A-596	Sequence 596, App
25	27	100.0	7	2	2	US-09-623-548A-607	Sequence 607, App
26	27	100.0	7	2	2	US-10-134-187-2	Sequence 2, Appli
27	27	100.0	7	2	2	US-09-657-276-596	Sequence 596, App
28	27	100.0	2	7	2	US-09-657-276-607	Sequence 607, Appl
29	27	100.0	2	1	2	US-07-737-371E-10	Sequence 10, Appl
30	27	100.0	2	1	1	US-07-737-371E-56	Sequence 56, Appl
31	27	100.0	2	1	2	US-09-623-548A-583	Sequence 583, Appl
32	27	100.0	2	1	2	US-09-623-548A-592	Sequence 592, Appl
33	27	100.0	2	1	2	US-09-623-548A-600	Sequence 600, Appl
34	27	100.0	2	1	2	US-09-657-276-583	Sequence 583, Appl
35	27	100.0	2	1	2	US-09-657-276-592	Sequence 592, Appl
36	27	100.0	2	1	2	US-09-657-276-600	Sequence 600, Appl
37	27	100.0	8	2	1	US-07-737-371E-60	Sequence 60, Appl
38	27	100.0	8	2	2	US-09-623-548A-545	Sequence 545, App
39	27	100.0	9	2	2	US-09-623-548A-622	Sequence 622, App
40	27	100.0	9	2	2	US-09-657-276-545	Sequence 545, App
41	27	100.0	9	2	2	US-09-657-276-622	Sequence 622, App
42	27	100.0	9	2	2	US-10-134-187-1	Sequence 1, Appli
43	27	100.0	10	1	2	US-08-088-322-6	Sequence 6, Appli
44	27	100.0	10	1	2	US-08-437-820-6	Sequence 6, Appli
45	27	100.0	10	1	1	US-07-737-371E-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-07-934-553-2
; Sequence 2, Application US/07934553
; Patent No. 5314690
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, ROY
; APPLICANT: HARRIS, KATHLEEN .E
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IgE
; TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TILTON, FALLON, LUNGMUS & CHESTNUT
; STREET: 100 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,553
; FILING DATE: 19920821
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/705,071
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTRESS, SUSAN B
; REGISTRATION NUMBER: 31,327
; REFERENCE/DOCKET NUMBER: NU-9033CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/456-8000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-07-934-553-2

Query Match   100.0%; Score 27; DB 1; Length 5;
Best Local Similarity   100.0%;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FFGLM 5
              |||||
Db   1 FFGLM 5

Db   1 FFGLM 5

RESULT 2
US-08-225-474-2
; Sequence 2, Application US/0822547474
; Patent No. 5560915
; GENERAL INFORMATION:
; APPLICANT: Patterson, Roy
; APPLICANT: Harris, Kathleen E.
; TITLE OF INVENTION: Method and Composition for Treating
; TITLE OF INVENTION: IgE Mediated Allergies
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
; STREET: 100 S. Wacker Drive, Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,474
; FILING DATE:
; PRIOR APPLICATION DATA:
; CLASSIFICATION: 514
; APPLICATION NUMBER: US 07/934,553
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/705,071
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tilton, Timothy L.
; REGISTRATION NUMBER: 16,926
; REFERENCE/DOCKET NUMBER: NU 9033-CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)-456-8000
; TELEFAX: (312)-456-7776
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-225-474-2

Qy   1 FFGLM 5
            |||||
Db   1 FFGLM 5

Query Match   100.0%; Score 27; DB 1; Length 5;
Best Local Similarity   100.0%; Pred. No. 4.6e+05;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 3
US-07-737-371E-6
; Sequence 6, Application US/07373771E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston

STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-737-371E-6

Qy   1 FFGLM 5
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Db   1 FFGLM 5

Query Match   100.0%; Score 27; DB 1; Length 5;
Best Local Similarity   100.0%; Pred. No. 4.6e+05;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 4
US-09-265-690C-1
; Sequence 1, Application US/09265690C
; Patent No. 6372440
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Me
; TITLE OF INVENTION: for Disease Diagnosis
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265,690C
; CURRENT FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
US-09-265-690C-1

Qy   1 FFGLM 5
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Db   1 FFGLM 5

Query Match   100.0%; Score 27; DB 2; Length 5;
Best Local Similarity   100.0%; Pred. No. 4.6e+05;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 5

OM protein - protein search, using sw model

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                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.
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Run on: November 26, 2005, 03:13:24 ; Search time 57.5 Seconds
                                                 (without alignments)
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Title: US-10-805-881-1
Perfect score: 27
Sequence: 1 FFGLM 5

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 439079

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :   Published_Applications_AA_Main:*
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                  2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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                  4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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                  6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	27	100.0	5	3	US-09-265-690C-1	Sequence 1, Appli
2	27	100.0	5	4	US-10-053-669-1	Sequence 1, Appli
3	27	100.0	5	4	US-10-134-187-3	Sequence 3, Appli
4	27	100.0	5	4	US-10-688-741-3	Sequence 3, Appli
5	27	100.0	5	4	US-10-805-881-1	Sequence 1, Appli
6	27	100.0	5	4	US-10-720-039-3	Sequence 3, Appli
7	27	100.0	5	5	US-10-497-628-15	Sequence 15, Appl
8	27	100.0	5	6	US-11-066-697-604	Sequence 604, App
9	27	100.0	6	5	US-11-025-494-3	Sequence 3, Appli
10	27	100.0	6	6	US-10-168-789A-38	Sequence 38, Appl
11	27	100.0	6	5	US-10-497-628-14	Sequence 14, Appl
12	27	100.0	6	6	US-11-066-697-595	Sequence 595, App
13	27	100.0	6	6	US-11-066-697-597	Sequence 597, App
14	27	100.0	6	6	US-11-066-697-601	Sequence 601, App
15	27	100.0	4	5	US-10-036-542-110	Sequence 110, App
16	27	100.0	4	5	US-10-036-542-111	Sequence 111, App
17	27	100.0	4	6	US-10-168-789A-37	Sequence 37, Appl
18	27	100.0	4	5	US-10-134-187-2	Sequence 2, Appli
19	27	100.0	4	4	US-10-688-741-2	Sequence 2, Appli
20	27	100.0	5	4	US-10-720-039-2	Sequence 2, Appli
21	27	100.0	5	6	US-11-066-697-596	Sequence 596, App
22	27	100.0	7	6	US-11-066-697-607	Sequence 607, App
23	27	100.0	7	5	US-10-497-628-13	Sequence 13, Appl
24	27	100.0	7	5	US-11-025-494-2	Sequence 2, Appli
25	27	100.0	8	6	US-10-168-789A-36	Sequence 36, Appl
26	27	100.0	5	6	US-10-497-628-12	Sequence 12, Appl
27	27	100.0	8	6	US-11-066-697-583	Sequence 583, App
28	27	100.0	5	6	US-11-066-697-592	Sequence 592, App
29	27	100.0	6	6	US-11-066-697-600	Sequence 600, App
30	27	100.0	6	3	US-10-036-542-112	Sequence 112, App
31	27	100.0	4	6	US-10-168-789A-35	Sequence 35, Appl
32	27	100.0	9	4	US-10-134-187-1	Sequence 1, Appli
33	27	100.0	9	4	US-10-688-741-1	Sequence 1, Appli
34	27	100.0	5	4	US-10-720-039-1	Sequence 1, Appli
35	27	100.0	5	6	US-11-066-697-545	Sequence 545, App
36	27	100.0	6	6	US-11-066-697-622	Sequence 622, App
37	27	100.0	6	5	US-10-168-789A-34	Sequence 34, Appl
38	27	100.0	6	5	US-11-025-494-1	Sequence 1, Appli
39	27	100.0	10	6	US-11-066-697-621	Sequence 621, App
40	27	100.0	10	6	US-11-079-147-71	Sequence 71, Appl
41	27	100.0	6	3	US-09-265-690C-3	Sequence 3, Appli
42	27	100.0	11	3	US-09-335-682-64	Sequence 64, Appl
43	27	100.0	11	3	US-09-841-091B-26	Sequence 26, Appl
44	27	100.0	11	3	US-09-988-792-1	Sequence 1, Appl
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ALIGNMENTS

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; Sequence 1, Application US/09265690C
; Publication No. US20010051345A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma_
; TITLE OF INVENTION: for Disease Diagnosis
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265,690C
; CURRENT FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.0
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; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
US-09-265-690C-1

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Best Local Similarity   100.0%;
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Qy          1 FFGLM 5
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Db          1 FFGLM 5

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; Sequence 1, Application US/10053669
; Publication No. US20030077658A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; TITLE OF INVENTION: for Disease Diagnosis
; FILE REFERENCE: N1427-005
; CURRENT APPLICATION NUMBER: US/10/053,669
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 09/265,690
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.0
;
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT

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;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (5)..(5)
;   OTHER INFORMATION: AMIDATION
US-10-053-669-1

Qy          1 FFGLM 5
              |||||
Db          1 FFGLM 5

RESULT 3
US-10-134-187-3
;   Sequence 3, Application US/10134187
;   Publication No. US20030202981A1
;   GENERAL INFORMATION:
;   APPLICANT: Kream, Richard M.
;   APPLICANT: Kream, Richard M.
;   APPLICANT: Kream, Richard M.
;   TITLE OF INVENTION: Chimeric Hybrid Analgesics
;   FILE REFERENCE: Kream
;   CURRENT APPLICATION NUMBER: US/10/134,187
;   CURRENT FILING DATE: 2002-04-26
;   NUMBER OF SEQ ID NOS: 3
;   SOFTWARE: Patentin version 3.1
;   SEQ ID NO 3
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: mammalian
US-10-134-187-3

Query Match           100.0%;  Score 27;  DB 4;  Length 5;
Best Local Similarity 100.0%;  Pred. No. 1.7e+06;
Matches  5;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy          1 FFGLM 5
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Db          1 FFGLM 5

RESULT 4
US-10-688-741-3
;   Sequence 3, Application US/10688741
;   Publication No. US20040106636A1
;   GENERAL INFORMATION:
;   APPLICANT: Kream, Richard M.
;   APPLICANT: Kream, Richard M.
;   APPLICANT: Kream, Richard M.
;   TITLE OF INVENTION: Method Of Inhibiting Opioid Tolerance Development With Chimeric H
;   TITLE OF INVENTION: Analgesics
;   FILE REFERENCE: Kream
;   CURRENT APPLICATION NUMBER: US/10/688,741
;   CURRENT FILING DATE: 2003-10-17
;   NUMBER OF SEQ ID NOS: 3
;   SOFTWARE: Patentin version 3.1
;   SEQ ID NO 3
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: mammalian
US-10-688-741-3

Query Match           100.0%;  Score 27;  DB 4;  Length 5;
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Matches  5;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Db          1 FFGLM 5
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US-10-805-881-1
;   Sequence 1, Application US/10805881
;   Publication No. US20040171093A1
;   GENERAL INFORMATION:
;   APPLICANT: Wells, Ibert C.
;   TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound
;   TITLE OF INVENTION: Magnesium for Disease Diagnosis
;   FILE REFERENCE: 800812-0005
;   CURRENT APPLICATION NUMBER: US/10/805,881
;   CURRENT FILING DATE: 2004-03-22
;   PRIOR APPLICATION NUMBER: US 10/053,669
;   PRIOR FILING DATE: 2002-01-24
;   PRIOR APPLICATION NUMBER: US 10/695,536
;   PRIOR FILING DATE: 2003-10-28
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: Patentin version 3.2
;   SEQ ID NO 1
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (5)..(5)
;   OTHER INFORMATION: AMIDATION
US-10-805-881-1

Query Match           100.0%;  Score 27;  DB 4;  Length 5;
Best Local Similarity 100.0%;  Pred. No. 1.7e+06;
Matches  5;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy          1 FFGLM 5
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Db          1 FFGLM 5

RESULT 6
US-10-720-039-3
;   Sequence 3, Application US/10720039
;   Publication No. US20040025978A1
;   GENERAL INFORMATION:
;   APPLICANT: Kream, Richard M.
;   APPLICANT: Kream, Richard M.
;   TITLE OF INVENTION: Method Of Transporting A Chimeric Hybrid Molecule Across The Bloo
;   TITLE OF INVENTION: Barrier
;   FILE REFERENCE: Kream
;   CURRENT APPLICATION NUMBER: US/10/720,039
;   CURRENT FILING DATE: 2003-11-20
;   NUMBER OF SEQ ID NOS: 3
;   SOFTWARE: Patentin version 3.1
;   SEQ ID NO 3
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: mammalian
US-10-720-039-3

Query Match           100.0%;  Score 27;  DB 5;  Length 5;
Best Local Similarity 100.0%;  Pred. No. 1.7e+06;
Matches  5;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy          1 FFGLM 5
              |||||
Db          1 FFGLM 5

RESULT 7
US-10-497-628-15
;   Sequence 15, Application US/10497628
;   Publication No. US20050009752A1
;   GENERAL INFORMATION:
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OM protein - protein search, using sw model

                    Copyright (c) 1993 - 2005 Compugen Ltd.
                    GenCore version 5.1.6

Run On:             November 26, 2005, 03:09:53 ; Search time 3.57143 Seconds
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                                                4.243 Million cell updates/sec

Title:              US-10-805-881-1
Perfect score:      27
Sequence:           1 FFGLM 5

Scoring table:      BLOSUM62
                    Gapop 10.0 , Gapext 0.5

Searched:           17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters:    7285

Post-processing: Minimum Match 0%
Maximum DB seq length: 0             Maximum Match 100%
Minimum DB seq length: 30            Listing first 45 summaries

Database :          Published Applications AA_New:*
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                    3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                    4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                    5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                    6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                    7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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SUMMARIES

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1    22     19    19    1    US-10-503-575-149        Sequence 149, Appl
2    20.4   19    19    1    US-11-054-515-2170       Sequence 2170, App
3    19     21    21    1    US-10-939-890-552        Sequence 552, Appl
4    18     11    7     1    US-11-054-515-3165       Sequence 3165, App
5    18     13    7     1    US-10-511-559-1043       Sequence 1043, Ap
6    18     13    7     1    US-10-511-559-1044       Sequence 1044, App
7    18     13    7     1    US-10-511-559-1045       Sequence 1045, Ap
8    18     13    7     1    US-10-511-559-1046       Sequence 1046, App
9    18     13    7     1    US-10-511-559-1047       Sequence 1047, Ap
10   18     13    7     1    US-10-511-559-1048       Sequence 1048, Ap
11   18     14    7     1    US-10-511-559-1322       Sequence 322, Appl
12   18     19    7     1    US-10-986-501-13         Sequence 13, Appl
13   18     19    7     1    US-11-038-501-13         Sequence 16, Appl
14   18     19    7     1    US-11-059-633-16         Sequence 16, Appl
15   18     21    7     1    US-10-939-890-509        Sequence 509, Appl
16   18     21    1     1    US-10-939-890-574        Sequence 574, App
17   17     8     1     1    US-10-939-890-517        Sequence 517, Appl
18   17     8     1     1    US-11-054-515-3098       Sequence 3098, App
19   17     12    7     1    US-11-054-515-2884       Sequence 2884, Ap
20   17     15    7     1    US-11-054-515-2976       Sequence 2976, Ap
21   17     16    7     1    US-11-054-515-3071       Sequence 3071, Ap
22   17     17    7     1    US-11-054-515-3025       Sequence 3025, Ap
23   17     18    7     1    US-11-054-515-2752       Sequence 2752, Ap
24   17     20    7     1    US-11-054-515-2802       Sequence 2802, Ap
25   16     8     7     1    US-11-044-051-80         Sequence 80, Appl
26   16     9     7     1    US-11-044-051-78         Sequence 78, Appl
27   16     9     7     1    US-11-044-051-79         Sequence 79, Appl
28   16     10    7     1    US-11-044-051-77         Sequence 77, Appl
29   16     10    7     1    US-11-044-051-85         Sequence 85, Appl
30   16     10    7     1    US-11-044-051-87         Sequence 87, Appl
31   16     10    7     1    US-11-044-051-88         Sequence 88, Appl
32   16     13    1     1    US-10-986-501-361        Sequence 361, App
33   16     13    1     1    US-10-939-890-192        Sequence 192, App
34   16     16    1     1    US-11-044-051-81         Sequence 81, Appl
35   16     16    7     1    US-11-054-515-2283       Sequence 2283, Ap
36   16     16    1     1    US-11-054-515-2893       Sequence 2893, Ap
37   16     16    7     1    US-10-503-575-161        Sequence 161, App
38   16     20    1     1    US-11-054-515-2865       Sequence 2865, Ap
39   16     21    7     1    US-11-022-562-125        Sequence 125, App
40   15     8     7     1    US-11-054-515-3132       Sequence 3132, Ap
41   15     12    7     1    US-10-923-605-4          Sequence 4, Appl
42   15     12    1     1    US-10-934-818-4          Sequence 4, Appli
43   15     13    1     1    US-10-511-559-478        Sequence 478, Appl
44   15     13    1     1    US-10-511-559-479        Sequence 479, App
45   15     13    1     1    US-10-511-559-480        Sequence 480, App
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ALIGNMENTS

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RESULT 1
US-10-503-575-149
; Sequence 149, Application US/10503575
; Publication No. US20050244823A1
; GENERAL INFORMATION:
;  APPLICANT: Drijfhout, Jan Wouter
;  APPLICANT: van Veelen, Petrus Antonius
;  APPLICANT: Koning, Frits
;  TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD.
;  TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS
;  FILE REFERENCE: 2799/72843-PCT-US
;  CURRENT APPLICATION NUMBER: US/10/503,575
;  CURRENT FILING DATE:
;  PRIOR APPLICATION NUMBER: 2004-08-04
;  PRIOR FILING DATE: PCT/NL03/00077
;  PRIOR APPLICATION NUMBER: 2003-02-04
;  PRIOR FILING DATE: EP 02075456.0
;  PRIOR APPLICATION NUMBER: 2002-02-04
;  NUMBER OF SEQ ID NOS: 340
;  SOFTWARE: Patentin version 3.1
; SEQ ID NO 149
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-575-149

Query Match             81.5%;  Score 22;  DB 1;  Length 19;
Best Local Similarity   100.0%;  Pred. No. 3.6;
Matches    4;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 FFGL 4
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Db         12 FFGL 15


RESULT 2
US-11-054-515-2170
; Sequence 2170, Application US/11054515
; Publication No. US20050255332A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE: 2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

RESULT 3
US-10-939-890-552
Sequence 552, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2170
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-054-515-2170

Query Match   70.4%; Score 19; DB 7; Length 19;
Best Local Similarity   75.0%; Pred. No. 19;
Matches   3; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

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Db   11 YFGL 14

; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
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NUMBER OF SEQ ID NOS: 3247

RESULT 4
US-11-054-515-3165
Sequence 3165, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
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; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
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; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3165
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-939-890-552

Query Match   70.4%; Score 19; DB 1; Length 21;
Best Local Similarity   80.0%; Pred. No. 21;
Matches   4; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 FFGLM 5
        |||:|
Db   10 FFGGM 14

; SEQ ID NO 552
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate

RESULT 5
US-10-511-559-1043
Sequence 1043, Application US/10511559
Publication No. US20050256304A1
GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII

US-11-054-515-3165

Query Match   66.7%; Score 18; DB 7; Length 11;
Best Local Similarity   100.0%; Pred. No. 19;
Matches   3; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FFG 3
        |||
Db   2 FFG 4

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: November 26, 2005, 01:57:32 ; Search time 182 Seconds
(without alignments)
12.071 Million cell updates/sec

Title: US-10-805-881-1
Perfect score: 27
Sequence: 1 FFGLM 5
Scoring table: BLOSUM62
Searched: Gapop 10.0 , Gapext 0.5
Total number of hits satisfying chosen parameters: 56929
2443163 seqs, 439378781 residues

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	27	100.0	5	2	AAR33009	Aar33009 Alpha-sub
2	27	100.0	5	2	AAR33008	Aar33008 Alpha-sub
3	27	100.0	5	2	AAR33007	Aar33007 Alpha-sub
4	27	100.0	5	2	AAR33010	Aar33010 Alpha-sub
5	27	100.0	5	2	AAR54549	Aar54549 Cholecyst
6	27	100.0	5	2	AAR54551	Aar54551 Cholecyst
7	27	100.0	5	2	AAR54550	Aar54550 Cholecyst
8	27	100.0	5	2	AAR54548	Aar54548 Cholecyst
9	27	100.0	5	2	AAW41687	Aaw41687 Tetrapept
10	27	100.0	5	2	AAW99643	Aaw99643 Neutrophi
11	27	100.0	5	2	AAY50325	Aay50325 Human tac
12	27	100.0	5	2	AAW92660	Aaw92660 Human/rat
13	27	100.0	5	3	AAB23025	Aab23025 Human tac
14	27	100.0	5	3	AAY67576	Aay67576 P antagon
15	27	100.0	5	4	AAB91428	Aab91428 Tachykini
16	27	100.0	5	5	ABB10088	Abb10088 Substance
17	27	100.0	5	5	AAU77845	Aau77845 Tachykini
18	27	100.0	5	7	ADE94203	Ade94203 High acti
19	27	100.0	5	7	ADF92530	Adf92530 Substance
20	27	100.0	5	8	ADN95078	Adn95078 Mammalian
21	27	100.0	5	8	ADR43771	Adr43771 Human mag
22	27	100.0	5	9	ADV44808	Adv44808 Mammalian
23	24	88.9	5	2	AAW92702	Aaw92702 Human tac
24	24	88.9	5	5	ABB10089	Abb10089 Substance
25	24	88.9	5	7	ADE94204	Ade94204 High acti
26	22	81.5	4	9	ADY04142	Ady04142 Peptide d
27	22	81.5	5	2	AAR27697	Aar27697 Cyclic ta
28	22	81.5	5	2	AAW92703	Aaw92703 Human tac
29	22	81.5	5	2	AAW92701	Aaw92701 Human tac
30	21	77.8	4	2	AAW41683	Aaw41683 Peptide u
31	21	77.8	4	2	AAY31075	Aay31075 Non-cross
32	21	77.8	4	3	AAB23026	Aab23026 Human/rat
33	21	77.8	4	4	AAY67577	Aay67577 Human/rat
34	21	77.8	4	5	AAB91447	Aab91447 Tachykini
35	21	77.8	4	5	ABB10091	Abb10091 Substance
36	21	77.8	4	5	AAU77846	Aau77846 Tachykini
37	21	77.8	4	7	ADE94198	Ade94198 High acti
38	21	77.8	4	8	ADR43772	Adr43772 Human mag
39	21	77.8	4	5	AAB91389	Aab91389 Tachykini
40	21	77.8	5	6	ABB10090	Abb10090 Substance
41	21	77.8	5	6	AAE35975	Aae35975 Zea mays
42	21	77.8	5	7	ADE94205	Ade94205 High acti
43	21	77.8	5	8	ADR03603	Adr03603 E. coli m
44	20	74.1	5	2	AAW80134	Aaw80134 COOH-term
45	20	74.1	5	2	AAR41695	Aar41695 GHRP-6 (G

ALIGNMENTS

RESULT 1
AAR33009
ID   AAR33009 standard; peptide; 5 AA.
XX
AC   AAR33009;
XX
DT   25-MAR-2003 (revised)
DT   02-APR-1993 (first entry)
XX
DE   Alpha-substituted short peptide.
XX
KW   CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
KW   improved bioavailability.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FH
FT   Modified-site 4
FT   /note= "alpha-Me-Leu"
FT   Modified-site 5
FT   /note= "Met-NH2"
XX
PN   WO9219254-A1.
XX
PD   12-NOV-1992.
XX
PF   15-APR-1992;   92WO-US003119.
XX
PR   20-MAR-1992;   92US-00852086.
PR   24-APR-1991;   91US-00690755.
XX
PT   New alpha-substd. polypeptide are e.g. selective receptor ligands - for
PT   treating inflammation, pain, stroke, ulcers, hypertension, heart failure,
PT   depression, cancer, asthma, psychosis, arthritis, etc.
XX
PA   (WARN) WARNER LAMBERT CO.
XX
PI   Horwell DC, Hughes J, Richardson RS, Howson W;
XX
DR   WPI; 1992-398522/48.
XX
PS   Claim 3; Page 41; 46pp; English.
XX
CC   The peptide is a specifically claimed example of a group of generically
CC   claimed mono-, di-, tri-, tetra- and penta-peptides which include a
CC   substituent on an alpha-C atom in the chain. Such substitution may modify
CC   the bioavailability, stability or absorbability of the peptide and hence

```
CC   may improve the activity of the peptide as a drug. Depending on the
CC   nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic
CC   peptide, etc.), the modified peptides are variously useful for treating
CC   obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,
CC   addictive drug withdrawal symptoms, hypertension, heart failure,
CC   cognition or memory disorders, spasticity, depression, diabetes, cancer,
CC   asthma, bladder dysfunction, psychosis and arthritis; and as
CC   contraceptives. (Updated on 25-MAR-2003 to correct PD field.) (Updated on
CC   25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct
CC   field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 5 AA;

Qy   1 FFGLM 5
       |||||
Db   1 FFGLM 5

Query Match             100.0%;  Score 27;  DB 2;  Length 5;
Best Local Similarity   100.0%;  Pred. No. 2e+06;
Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

RESULT 2
AAR33008
ID   AAR33008 standard; peptide; 5 AA.
XX
AC   AAR33008;
XX
DT   25-MAR-2003  (revised)
DT   02-APR-1993  (first entry)
XX
DE   Alpha-substituted short peptide.
XX
KW   CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
KW   improved bioavailability.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   2
FT                   /note= "alpha-Me-Phe"
FT   Modified-site   5
FT                   /note= "Met-NH2"
XX
PN   WO9219254-A1.
XX
PD   12-NOV-1992.
XX
PF   15-APR-1992;  92WO-US003119.
XX
PR   24-APR-1991;  91US-00690755.
PR   20-MAR-1992;  92US-00852086.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Horwell DC, Hughes J, Richardson RS, Howson W;
XX
DR   WPI; 1992-398522/48.
XX
PT   New alpha-substd. polypeptide are e.g. selective receptor ligands - for
PT   treating inflammation, pain, stroke, ulcers, hypertension, heart failure,
PT   depression, cancer, asthma, psychosis, arthritis, etc.
XX
PS   Claim 3; Page 41; 46pp; English.
XX
CC   The peptide is a specifically claimed example of a group of generically
CC   claimed mono-, di-, tri-, tetra- and penta-peptides which include a
CC   substituent on an alpha-C atom in the chain. Such substitution may modify
CC   the bioavailability, stability or absorbability of the peptide and hence
CC   may improve the activity of the peptide as a drug. Depending on the
CC   nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic
CC   peptide, etc.), the modified peptides are variously useful for treating
CC   obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,
```

```
CC   addictive drug withdrawal symptoms, hypertension, heart failure,
CC   cognition or memory disorders, spasticity, depression, diabetes, cancer,
CC   asthma, bladder dysfunction, psychosis and arthritis; and as
CC   contraceptives. (Updated on 25-MAR-2003 to correct PD field.) (Updated on
CC   25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PR
CC   field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 5 AA;

Qy   1 FFGLM 5
       |||||
Db   1 FFGLM 5

Query Match             100.0%;  Score 27;  DB 2;  Length 5;
Best Local Similarity   100.0%;  Pred. No. 2e+06;
Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

RESULT 3
AAR33007
ID   AAR33007 standard; peptide; 5 AA.
XX
AC   AAR33007;
XX
DT   25-MAR-2003  (revised)
DT   02-APR-1993  (first entry)
XX
DE   Alpha-substituted short peptide.
XX
KW   CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
KW   improved bioavailability.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "alpha-Me-Phe"
FT   Modified-site   5
FT                   /note= "Met-NH2"
XX
PN   WO9219254-A1.
XX
PD   12-NOV-1992.
XX
PF   15-APR-1992;  92WO-US003119.
XX
PR   24-APR-1991;  91US-00690755.
PR   20-MAR-1992;  92US-00852086.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Horwell DC, Hughes J, Richardson RS, Howson W;
XX
DR   WPI; 1992-398522/48.
XX
PT   New alpha-substd. polypeptide are e.g. selective receptor ligands - for
PT   treating inflammation, pain, stroke, ulcers, hypertension, heart failure,
PT   depression, cancer, asthma, psychosis, arthritis, etc.
XX
PS   Claim 3; Page 41; 46pp; English.
XX
CC   The peptide is a specifically claimed example of a group of generically
CC   claimed mono-, di-, tri-, tetra- and penta-peptides which include a
CC   substituent on an alpha-C atom in the chain. Such substitution may modify
CC   the bioavailability, stability or absorbability of the peptide and hence
CC   may improve the activity of the peptide as a drug. Depending on the
CC   nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic
CC   peptide, etc.), the modified peptides are variously useful for treating
CC   obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,
CC   addictive drug withdrawal symptoms, hypertension, heart failure,
CC   cognition or memory disorders, spasticity, depression, diabetes, cancer,
CC   asthma, bladder dysfunction, psychosis and arthritis; and as
CC   contraceptives. (Updated on
```

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: November 26, 2005, 02:09:53 ; Search time 38 Seconds
(without alignments)
12.660 Million cell updates/sec

Title: US-10-805-881-1
Perfect score: 27
Sequence: 1 FFGLM 5
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621676 3 residues

Total number of hits satisfying chosen parameters: 206

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	66.7	5	2	PT0278	Ig heavy chain CRD
2	14	51.9	5	2	A44955	alkanal monooxygen
3	12	44.4	4	2	JQ1273	neuropeptide Antho
4	11	40.7	4	2	A61445	Met-enkephalin - b
5	11	40.7	4	2	PT0244	Ig heavy chain CRD
6	10	37.0	4	2	A53284	T-cell receptor be
7	10	37.0	4	2	G44817	27.5 kda structura
8	10	37.0	4	2	I44817	27.5K structural p
9	10	37.0	5	2	E44817	28.5K structural p
10	10	37.0	5	2	C44817	28.5K structural p
11	10	37.0	5	2	A44817	28K structural pro
12	9	33.3	3	2	S68328	blood cell protein
13	9	33.3	3	2	A32516	cholecystokinin-5
14	9	33.3	5	2	PQ0689	photosystem I 10.4
15	8	33.3	5	2	B61445	Leu-enkephalin - b
16	8	29.6	2	2	PT0633	T-cell receptor be
17	8	29.6	3	2	PT0572	T-cell receptor be
18	8	29.6	3	2	B23751	spinal cord peptid
19	7	25.9	4	2	E44823	synaptosomal-assoc
20	7	25.9	2	2	B53284	T-cell receptor be
21	7	25.9	5	2	T10954	hypothetical prote
22	7	25.9	5	2	JH0253	gut pentapeptide -
23	7	25.9	5	2	S69237	surface protein te
24	6	22.2	3	3	PT0636	T-cell receptor be
25	6	22.2	3	3	PT0571	T-cell receptor be
26	6	22.2	3	3	GKHU	growth-modulating
27	6	22.2	3	3	A60898	bursin - chicken
28	6	22.2	3	3	A2751	spinal cord peptid
29	6	22.2	4	1	ECXAA	antho-RFamide neur
30	6	22.2	4	2	D41654	hypothetical prote
31	6	22.2	4	2	S53508	starvation-induced
32	6	22.2	4	2	T30569	hypothetical prote
33	6	22.2	4	2	138888	COI intron 16 prot
34	6	22.2	4	2	A25844	auto-RF amide neu
35	6	22.2	4	2	A34626	RPCH-related neuro
36	6	22.2	4	2	S39390	Ig mu chain V regi
37	6	22.2	4	2	S43959	myosin-light-chain
38	6	22.2	4	2	S47552	ubiquitin - rat
39	6	22.2	4	2	S09478	globulin IV alpha
40	6	22.2	4	2	PL0140	carbon-monoxide de
41	6	22.2	4	2	A35779	neuropeptide Antho
42	6	22.2	4	2	A60418	FMRFamide - polych
43	6	22.2	4	2	A32480	achatin-I - giant
44	6	22.2	4	2	PT0271	Ig heavy chain CRD
45	6	22.2	4	1	PT0711	T-cell receptor be

ALIGNMENTS

RESULT 1
PT0278
Ig heavy chain CRD3 region (clone 4-88) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0278
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0278
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
A;Cross-references: UNIPARC:UPI000017C202
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match   66.7%; Score 18; DB 2; Length 5;
Best Local Similarity   40.0%; Pred. No. 2.8e+05;
Matches   2; Conservative   3; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FFGLM 5
           :||||:
Db   1 YFGVL 5

RESULT 2
A44955
alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) alpha chain - Vibrio harveyi (fragment
C;Species: Vibrio harveyi
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000
C;Accession: A44955
R;Paquatte, O.; Tu, S.C.
Photochem. Photobiol. 50, 817-825, 1989
A;Title: Chemical modification and characterization of the alpha cysteine 106 at the vib
A;Reference number: A44955; MUID:90175700; PMID:2626493
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <PAQ>
A;Cross-references: UNIPARC:UPI0000017AAD8
C;Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match   51.9%; Score 14; DB 2; Length 5;
Best Local Similarity   66.7%; Pred. No. 2.8e+05;
Matches   2; Conservative   1; Mismatches   0; Gaps   0;

Qy   2 FGL 4
           ||:
Db   1 FGI 3

RESULT 3
JQ1273

C;neuropeptide Antho-KAamide - sea anemone (Anthopleura elegantissima)
C;Species: Anthopleura elegantissima
A;Title: Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a novel neuropep
A;Reference number: JQ1273; MUID:92028852; PMID:1681803
A;Accession: JQ1273
A;Molecule type: protein
R;Nothacker, H.P.; Rinehart, K.L.; Grimmelikhuijzen, C.J.P.
Biochem. Biophys. Res. Commun. 179, 1205-1211, 1991
C;Accession: JQ1273
C;Date: 31-Mar-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
A;Residues: 1-4 <NOT>
A;Cross-references: UNIPROT:P58705; UNIPARC:UPI000012A703
C;Comment: The carboxyl-terminal amide probably arises from cleavage of a following glyc
F;1/Modified site: amidated carboxyl end; neuropeptide; phenyllactylation
F;3/Modified site: L-3-phenyllactic acid (Phe) #status experimental
F;4/Modified site: amidated carboxyl end (Ala) #status experimental

Query Match　　44.4%; Score 12; DB 2; Length 4;
Best Local Similarity　100.0%; Pred. No. 2.8e+05;
Matches　2; Conservative　0; Mismatches　0; Indels　0; Gaps　0;

Qy　1 FF 2
　　||
Db　1 FF 2

RESULT 4
A61445

Met-enkephalin - blue mussel
C;Species: Mytilus edulis (blue mussel)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
A;Accession: A61445
A;Molecule type: protein
R;Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A;Reference number: A61445; MUID:84144823; PMID:6583690
A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis
A;Accession: A61445
A;Molecule type: protein
A;Residues: 1-5 <LEU>
A;Cross-references: UNIPARC:UPI000002CF9B
A;Experimental source: pedal ganglia
C;Keywords: neuropeptide; opioid peptide

Query Match　　40.7%; Score 11; DB 2; Length 5;
Best Local Similarity　66.7%; Pred. No. 2.8e+05;
Matches　2; Conservative　0; Mismatches　1; Indels　0; Gaps　0;

Qy　3 GL 5
　　| |
Db　3 GFM 5

RESULT 5
PT0240

Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0240
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0240
A;Molecule type: DNA
A;Residues: 1-4 <YAM>
A;Cross-references: UNIPARC:UPI00017C1E2
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match　　37.0%; Score 10; DB 2; Length 4;
Best Local Similarity　100.0%; Pred. No. 2.8e+05;

Matches　2; Conservative　0; Mismatches　0; Indels　0; Gaps　0;

Qy　3 GL 4
　　||
Db　3 GL 4

RESULT 6
A53284

T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
A;Accession: A53284
R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A;Title: Evolutionarily conserved organization and sequences of germline diversity and j
A;Reference number: A53284; MUID:91342695; PMID:1678859
A;Accession: A53284
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4 <HAR>
A;Cross-references: UNIPARC:UPI00011E8F2; GB:S60737; NID:g233916; PIDN:AAB19517.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60739)
C;Keywords: T-cell receptor

Query Match　　37.0%; Score 10; DB 2; Length 4;
Best Local Similarity　100.0%; Pred. No. 2.8e+05;
Matches　2; Conservative　0; Mismatches　0; Indels　0; Gaps　0;

Qy　3 GL 4
　　||
Db　1 GL 2

RESULT 7
G44817

27.5 kda structural protein - Leuconostoc oenos phage P32 (fragment)
C;Species: Leuconostoc oenos phage P37
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: G44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: G44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Cross-references: UNIPARC:UPI00017CA3A
A;Note: sequence extracted from NCBI backbone (NCBIP:70333)

Query Match　　37.0%; Score 10; DB 2; Length 5;
Best Local Similarity　100.0%; Pred. No. 2.8e+05;
Matches　2; Conservative　0; Mismatches　0; Indels　0; Gaps　0;

Qy　3 GL 4
　　||
Db　4 GL 5

RESULT 8
I44817

27.5K structural protein - Leuconostoc oenos phage P37 (fragment)
C;Species: Leuconostoc oenos phage P37
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: I44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: I44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Cross-references: UNIPARC:UPI00017CA3A

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: November 26, 2005, 02:06:57 ; Search time 225 Seconds
(without alignments)
15.678 Million cell updates/sec

Title: US-10-805-881-1
Perfect score: 27
Sequence: 1 FFGLM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 60

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length DB		ID	Description
1	16	59.3	5	1	ALL14_CARMA	carcinus ma
2	12	44.4	4	1	FFKA_ANTEL	anthopleura
3	12	44.4	4	1	OCP1_OCTMI	octopus min
4	12	44.4	5	1	P8648	pardachirus
5	12	44.4	5	1	PAP2_PARMA	
6	12	44.4	5	1	RBE1_LITRU	litoria rub
7	12	44.4	5	1	RBE21_LITRU	litoria rub
8	12	44.4	5	1	RBE31_LITRU	litoria rub
9	12	44.4	5	1	RBE32_LITRU	litoria rub
10	11	40.7	5	1	UC22_MAIZE	zea mays (m
11	9	33.3	4	1	TPIS_CANFA	canis famil
12	9	33.3	4	1	FYRI_ANTEL	anthopleura
13	7	25.9	4	1	ILME_SEPOF	sepia offic
14	6	22.2	2	1	UF01_MOUSE	mus musculu
15	6	22.2	3	1	GWA_SEPOF	sepia offic
16	6	22.2	2	1	GRWM_HUMAN	homo sapien
17	6	22.2	4	1	ACH1_ACHFU	achatina fu
18	6	22.2	4	1	DCML_PSECH	pseudomonas
19	6	22.2	4	1	EOSI_HUMAN	homo sapien
20	6	22.2	4	1	FAR3_HIRME	hirudo medi
21	6	22.2	4	1	FAR4_HIRME	hirudo medi
22	6	22.2	4	1	FLRF_HELTI	helisoma tr
23	6	22.2	4	1	FLRF_HIRME	hirudo medi
24	6	22.2	4	1	FLRN_ANTEL	anthopleura
25	6	22.2	4	1	FMRF_HELTI	helisoma tr
26	6	22.2	4	1	FMRF_HIRME	hirudo medi
27	6	22.2	4	1	FMRF_MACNI	macrocallis
28	6	22.2	4	1	FMRF_NERVI	nereis vire
29	6	22.2	4	1	OCP3_OCTMI	octopus min
30	6	22.2	4	2	TPANI_PANIM	pandinus im
31	6	22.2	5	1	Q16047_HUMAN	homo sapien
32	6	22.2	5	1	AP21_EISFO	eisenia foe
33	6	22.2	5	1	EI03_LITRU	litoria rub
34	6	22.2	5	1	EI04_LITRU	litoria rub
35	6	22.2	5	1	FARP_ARTTR	artioposthi
36	6	22.2	5	1	FARP_CHICK	gallus gall
37	6	22.2	5	1	SUGA_ACHDO	achaeta dome
38	5	18.5	4	1	UXA4_CHLTR	chlamydia t
39	5	18.5	4	2	DCMS_PSECH	pseudomonas
40	5	18.5	5	1	Q96AT0_HUMAN	homo sapien
41	5	18.5	5	1	BIOA_CITFR	citrobacter
42	5	18.5	5	1	BIOB_CITFR	citrobacter
43	5	18.5	5	2	RPC2_BPP21	
44	5	18.5	5	1	Q99007_HORVU	hordeum vul
44	5	18.5	5	2	P83073_BACCE	bacillus ce
45	4	14.8	4	1	TPAN2_PANIM	pandinus im

ALIGNMENTS

RESULT 1
ALL14_CARMA

ID   ALL14_CARMA   STANDARD;   PRT;   5 AA.
AC   P81817;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Carcinustatin-14.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the allatostatin family.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
KW   Amidation; Direct protein sequencing; Multigene family; Neuropeptide.
FT   MOD_RES   5   5   Leucine amide (Potential).
SQ   SEQUENCE   5 AA;   586 MW;   672879D5AB300000 CRC64;

Query Match   59.3%; Score 16; DB 1; Length 5;
Best Local Similarity   100.0%; Pred. No. 2.2e+06;
Matches   3; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 FGL 4
              |||
Db   3 FGL 5

RESULT 2
FFKA_ANTEL

ID   FFKA_ANTEL   STANDARD;   PRT;   4 AA.
AC   P58705;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Antho-KAamide.
OS   Anthopleura elegantissima (Sea anemone).

```
OC   Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC   Nynantheae; Actiniidae; Anthopleura.
OX   NCBI_TaxID=6110;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=92028852; PubMed=1681803;
RA   Nothacker H.-P., Rinehart K.L.Jr., Grimelikhuijzen C.J.P.;
RT   "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a
RT   novel neuropeptide from sea anemones.";
RL   Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
RN   [2]
RP   FUNCTION.
RX   MEDLINE=9391436; PubMed=8397415;
RA   McFarlane I.D., Hudman D., Nothacker H.-P., Grimelikhuijzen C.J.P.;
RT   "The expansion behaviour of sea anemones may be coordinated by two
RT   inhibitory neuropeptides, Antho-KAamide and Antho-RIamide.";
RL   Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC   -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC       groups. May be involved in the expansion phase of feeding
CC       behaviour in sea anemones.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Neuron specific.
```
```
DR   PIR; JQ1273; JQ1273.
KW   Amidation; Direct protein sequencing; Neuropeptide.
FT   MOD_RES       1      1       3-phenyllactic acid.
FT   MOD_RES       4      4       Alanine amide.
SQ   SEQUENCE   4 AA;  512 MW;  6D339C9A0000000 CRC64;

Query Match             44.4%;  Score 12;  DB 1;  Length 4;
Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
Matches    2; Conservative    0; Mismatches   0; Indels   0; Gaps   0;

Qy           1 FF 2
               ||
Db           1 FF 2


RESULT 3
ID   OCP1_OCTMI     STANDARD;      PRT;    4 AA.
AC   P58648;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Cardioactive peptides Ocp-1/Ocp-2.
OS   Octopus minor (Octopus).
OC   Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC   Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX   NCBI_TaxID=89766;
RN   [1]
RP   PROTEIN SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC   TISSUE=Brain;
RX   MEDLINE=20336815; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;
RA   Iwakoshi E., Hisada M., Minakata H.;
RT   "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT   Octopus minor.";
RL   Peptides 21:623-630(2000).
CC   -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC       inotropic effects on the heart. Ocp-2 is a 1000 time less active
CC       than Ocp-1.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: Ocp-2 has L-Phe instead of D-Phe.
CC   -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.
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```
KW   D-amino acid; Direct protein sequencing; Hormone.
FT   MOD_RES       2      2       D-phenylalanine (in form Ocp-1).
FT   MOD_RES       2      2       D-phenylalanine.
SQ   SEQUENCE   4 AA;  394 MW;  6AA879C810000000 CRC64;

Query Match             44.4%;  Score 12;  DB 1;  Length 4;
Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
Matches    2; Conservative    0; Mismatches   0; Indels   0; Gaps   0;

Qy           2 FG 3
               ||
Db           2 FG 3


RESULT 4
ID   PAP2_PARMA     STANDARD;      PRT;    5 AA.
AC   P81864;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Pardaxin II (PXII) (Fragment).
OS   Pardachirus marmoratus (Red sea moses sole).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC   Soleoidei; Soleidae; Pardachirus.
OX   NCBI_TaxID=31087;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Skin secretion;
RX   MEDLINE=87057369; PubMed=3782138;
RA   Lazarovici P., Primor N., Loew L.M.;
RT   "Purification and pore-forming activity of two hydrophobic
RT   polypeptides from the secretion of the Red sea moses sole (Pardachirus
RT   marmoratus).";
RL   J. Biol. Chem. 261:16704-16713(1986).
CC   -!- FUNCTION: Exhibits unusual shark repellent and surfactant
CC       properties. Forms voltage-dependent, ion-permeable channels in
CC       membranes. At high concentration causes cell membrane lysis.
CC   -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pardaxin family.
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KW   Direct protein sequencing; Toxin.
FT   NON_TER       5      5
SQ   SEQUENCE   5 AA;  614 MW;  7769C9C8100000000 CRC64;

Query Match             44.4%;  Score 12;  DB 1;  Length 5;
Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
Matches    2; Conservative    0; Mismatches   0; Indels   0; Gaps   0;

Qy           1 FF 2
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Db           2 FF 3


RESULT 5
ID   RBE11_LITRU    STANDARD;      PRT;    5 AA.
AC   P82070;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   01-FEB-2005 (Rel. 46, Last annotation update)
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OM protein - protein search, using sw model

Run on: November 26, 2005, 02:07:07 ; Search time 45 Seconds
(without alignments)
9.186 Million cell updates/sec

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Title: US-10-805-881-1
Perfect score: 27
Sequence: 1 FFGLM 5
Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5
Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 30800

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents AA:*
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3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	27	100.0	5	1	US-07-934-553-2	Sequence 2, Appli
2	27	100.0	5	2	US-08-225-474-2	Sequence 2, Appli
3	27	100.0	5	1	US-07-737-371E-6	Sequence 6, Appli
4	27	100.0	5	2	US-09-265-690C-1	Sequence 1, Appli
5	27	100.0	5	2	US-09-623-548A-604	Sequence 604, App
6	27	100.0	5	2	US-10-134-187-3	Sequence 3, Appli
7	27	100.0	5	2	US-09-657-276-604	Sequence 604, App
8	24	88.9	5	2	US-07-737-371E-48	Sequence 48, Appl
9	22	81.5	5	1	US-07-737-371E-47	Sequence 47, Appl
10	22	81.5	5	1	US-07-737-371E-49	Sequence 49, Appl
11	21	77.8	5	4	US-08-441-591-63	Sequence 63, Appl
12	21	77.8	5	1	US-08-303-362A-63	Sequence 63, Appl
13	21	77.8	5	2	US-09-265-690C-2	Sequence 2, Appli
14	21	77.8	5	2	US-10-230-133-3	Sequence 3, Appli
15	21	77.8	5	2	US-09-635-266-3	Sequence 3, Appli
16	21	77.8	5	2	US-09-623-548A-623	Sequence 623, App
17	21	77.8	5	2	US-09-657-276-623	Sequence 623, App
18	21	77.8	5	4	US-10-695-536-3	Sequence 3, Appli
19	21	77.8	5	2	US-08-070-301-6	Sequence 6, Appl
20	21	77.8	5	2	US-09-623-548A-565	Sequence 565, App
21	21	77.8	5	2	US-09-657-276-565	Sequence 565, App
22	21	77.8	5	2	US-07-753-909B-3	Sequence 3, Appli
23	20	74.1	5	2	US-08-269-288-1	Sequence 1, Appli
24	20	74.1	5	1	US-08-391-910-1	Sequence 1, Appli
25	20	74.1	5	1	US-08-418-994-1	Sequence 1, Appli
26	20	74.1	5	1	US-08-391-814-1	Sequence 1, Appli
27	20	74.1	5	1	US-08-391-814-1	Sequence 1, Appli
28	20	74.1	5	1	US-08-441-591-61	Sequence 61, Appl
29	20	74.1	5	1	US-08-303-362A-61	Sequence 61, Appl
30	20	74.1	5	1	US-08-462-415-1	Sequence 1, Appli
31	20	74.1	5	1	US-08-463-874-1	Sequence 1, Appli
32	20	74.1	5	1	US-08-444-135-1	Sequence 1, Appli
33	20	74.1	5	1	US-08-318-391-1	Sequence 1, Appli
34	20	74.1	5	2	US-08-257-966-1	Sequence 4, Appli
35	20	74.1	5	2	US-09-265-690C-4	Sequence 4, Appl
36	20	74.1	5	2	US-08-153-847-1	Sequence 1, Appli
37	20	74.1	5	1	US-09-635-266-4	Sequence 4, Appl
38	20	74.1	5	4	US-10-230-133-4	Sequence 4, Appli
39	20	74.1	5	2	US-10-695-536-4	Sequence 4, Appl
40	20	74.1	5	1	US-10-668-565-1	Sequence 1, Appl
41	20	74.1	5	4	PCT-US95-05600-78	Sequence 78, Appl
42	19	70.4	5	2	US-08-722-126A-20	Sequence 20, Appli
43	19	70.4	5	1	US-10-765-061-5	Sequence 5, Appl
44	19	70.4	5	2	US-09-623-548A-606	Sequence 606, App
45	19	70.4	5	2	US-09-657-276-606	Sequence 606, App

ALIGNMENTS

RESULT 1
US-07-934-553-2
Sequence 2, Application US/07934553
; Patent No. 5314690
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, ROY
; APPLICANT: HARRIS, KATHLEEN E
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IgE
; TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TILTON, FALLON, LUNGMUS & CHESTNUT
; STREET: 100 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,553
; FILING DATE: 19920821
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/705,071
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTRESS, SUSAN B
; REGISTRATION NUMBER: 31,327
; REFERENCE/DOCKET NUMBER: NU-9033CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/456-8000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-07-934-553-2

Query Match 100.0%; Score 27; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 FFGLM 5
            |||||

Db 1 FFGLM 5

RESULT 2
US-08-225-474-2
Sequence 2, Application US/0822547A
Patent No. 5560915
; GENERAL INFORMATION:
; APPLICANT: Patterson, Roy
; APPLICANT: Harris, Kathleen E.
; TITLE OF INVENTION: Method and Composition for Treating
; TITLE OF INVENTION: IgE Mediated Allergies
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
; STREET: 100 S. Wacker Drive, Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,474
; FILING DATE:
; PRIOR APPLICATION DATA:
; CLASSIFICATION: 514
; APPLICATION NUMBER: US 07/934,553
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/705,071
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tilton, Timothy L.
; REGISTRATION NUMBER: 16,926
; REFERENCE/DOCKET NUMBER: NU 9033-CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)-456-8000
; TELEFAX: (312)-456-7776
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-225-474-2

Query Match   100.0%; Score 27; DB 1; Length 5;
Best Local Similarity   100.0%; Pred. No. 4.6e+05;
Matches   5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 FFGLM 5
              |||||
Db   1 FFGLM 5

RESULT 3
US-07-737-371E-6
Sequence 6, Application US/07373371E
Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston

; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-737-371E-6

Query Match   100.0%; Score 27; DB 1; Length 5;
Best Local Similarity   100.0%; Pred. No. 4.6e+05;
Matches   5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 FFGLM 5
              |||||
Db   1 FFGLM 5

RESULT 4
US-09-265-690C-1
Sequence 1, Application US/09265690C
Patent No. 6372440
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Me
; TITLE OF INVENTION: for Disease Diagnosis
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265,690C
; CURRENT FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
US-09-265-690C-1

Query Match   100.0%; Score 27; DB 2; Length 5;
Best Local Similarity   100.0%; Pred. No. 4.6e+05;
Matches   5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 FFGLM 5
              |||||
Db   1 FFGLM 5

RESULT 5

OM protein - protein search, using sw model

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Run on: November 26, 2005, 02:17:08 ; Search time 158 Seconds
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Title: US-10-805-881-1
Perfect score: 27
Sequence: 1 FFGLM 5
Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 31220

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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  4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
  5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
  6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	27	100.0	5	3	US-09-265-690C-1	Sequence 1, Appli
2	27	100.0	5	4	US-10-053-669-1	Sequence 1, Appli
3	27	100.0	5	4	US-10-134-187-3	Sequence 3, Appli
4	27	100.0	5	4	US-10-688-741-1	Sequence 3, Appli
5	27	100.0	5	5	US-10-805-881-1	Sequence 1, Appli
6	27	100.0	5	5	US-10-720-039-3	Sequence 3, Appli
7	27	100.0	5	5	US-10-805-881-2	Sequence 3, Appli
8	27	100.0	5	4	US-11-066-697-604	Sequence 15, Appli
9	27	100.0	5	6	US-11-066-697-604	Sequence 604, Appli
10	24	100.0	5	6	US-11-025-494-3	Sequence 3, Appli
11	22	88.9	5	5	US-10-497-628-16	Sequence 16, Appli
12	22	81.5	4	5	US-10-821-240A-270	Sequence 270, App
13	21	77.8	4	3	US-09-265-690C-2	Sequence 2, Appli
14	21	77.8	4	4	US-10-230-133-3	Sequence 2, Appli
15	21	77.8	4	5	US-10-053-669-2	Sequence 2, Appli
16	21	77.8	4	5	US-10-695-536-3	Sequence 3, Appli
17	21	77.8	4	6	US-10-805-881-2	Sequence 2, Appli
18	21	77.8	4	6	US-10-497-628-2	Sequence 2, Appli
19	21	77.8	4	6	US-11-018-690-3	Sequence 3, Appli
20	21	77.8	4	5	US-11-066-697-623	Sequence 623, Appl
21	21	77.8	5	5	US-10-346-737A-30	Sequence 30, Appl
22	21	77.8	4	5	US-10-497-628-17	Sequence 17, Appl
23	21	77.8	3	5	US-11-066-697-565	Sequence 565, App
24	20	74.1	4	5	US-09-265-690C-4	Sequence 4, Appli
25	20	74.1	4	5	US-10-230-133-4	Sequence 4, Appli
26	20	74.1	5	5	US-10-695-536-4	Sequence 4, Appli
27	20	74.1	5	4	US-10-805-881-4	Sequence 4, Appli
28	20	74.1	5	6	US-10-451-304-12	Sequence 12, Appl
29	20	74.1	5	6	US-11-018-690-4	Sequence 4, Appli
30	20	70.4	4	5	US-10-346-737A-22	Sequence 22, Appl
31	19	70.4	5	6	US-11-066-697-1527	Sequence 1527, Ap
32	18	66.7	3	6	US-11-066-697-1527	Sequence 1527, Ap
33	18	66.7	4	2	US-08-484-409-14	Sequence 14, Appl
34	18	66.7	4	4	US-10-155-170-4	Sequence 4, App
35	18	66.7	4	4	US-10-351-641-826	Sequence 826, App
36	18	66.7	4	4	US-10-822-661-4	Sequence 4, Appli
37	18	66.7	4	5	US-10-821-240A-298	Sequence 298, Appl
38	18	66.7	4	5	US-10-878-175B-3	Sequence 3, Appl
39	18	66.7	5	5	US-09-920-306-38	Sequence 38, Appl
40	17	63.0	5	5	US-10-168-789A-32	Sequence 32, Appl
41	17	63.0	5	5	US-10-783-311-299	Sequence 299, App
42	16	59.3	4	3	US-09-879-442A-9	Sequence 9, Appli
43	16	59.3	5	3	US-09-886-135-2	Sequence 2, Appli
44	16	59.3	5	4	US-10-620-052A-45	Sequence 45, Appli
45	16	59.3	5	4	US-10-337-105-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-265-690C-1

; Sequence 1, Application US/09265690C
; Publication No. US20010051345A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
; TITLE OF INVENTION: for Disease Diagnosis
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265,690C
; CURRENT FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.0
;
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
US-09-265-690C-1

  Query Match   100.0%; Score 27; DB 3; Length 5;
  Best Local Similarity   100.0%;
  Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FFGLM 5
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Db   1 FFGLM 5

RESULT 2
US-10-053-669-1
; Sequence 1, Application US/10053669
; Publication No. US20030077658A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
; TITLE OF INVENTION: for Disease Diagnosis
; FILE REFERENCE: N1427-005
; CURRENT APPLICATION NUMBER: US/10/053,669
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 09/265,690
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.0
;
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT

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;   ORGANISM: Homo sapiens
;   FEATURE:
;     NAME/KEY: MOD_RES
;     LOCATION: (5)..(5)
;     OTHER INFORMATION: AMIDATION
US-10-053-669-1

Qy        1 FFGLM 5
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Db        1 FFGLM 5


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Best Local Similarity 100.0%;    Pred. No. 1.7e+06;
Matches    5;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;


RESULT 3
US-10-134-187-3
;   Sequence 3, Application US/10134187
;   Publication No. US20030202981A1
;   GENERAL INFORMATION:
;   APPLICANT: Kream, Richard M.
;   APPLICANT: Kream, Richard M.
;   APPLICANT: Kream, Richard M.
;   TITLE OF INVENTION: Chimeric Hybrid Analgesics
;   FILE REFERENCE: Kream
;   CURRENT APPLICATION NUMBER: US/10/134,187
;   CURRENT FILING DATE: 2002-04-26
;   NUMBER OF SEQ ID NOS: 3
;   SOFTWARE: Patentin version 3.1
;   SEQ ID NO 3
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: mammalian
US-10-134-187-3

Qy        1 FFGLM 5
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Db        1 FFGLM 5


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Best Local Similarity 100.0%;    Pred. No. 1.7e+06;
Matches    5;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;


RESULT 4
US-10-688-741-3
;   Sequence 3, Application US/10688741
;   Publication No. US20040106636A1
;   GENERAL INFORMATION:
;   APPLICANT: Kream, Richard M.
;   APPLICANT: Kream, Richard M.
;   APPLICANT: Kream, Richard M.
;   TITLE OF INVENTION: Method Of Inhibiting Opioid Tolerance Development With Chimeric H
;   TITLE OF INVENTION: Analgesics
;   FILE REFERENCE: Kream
;   CURRENT APPLICATION NUMBER: US/10/688,741
;   CURRENT FILING DATE: 2003-10-17
;   NUMBER OF SEQ ID NOS: 3
;   SOFTWARE: Patentin version 3.1
;   SEQ ID NO 3
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: mammalian
US-10-688-741-3

Qy        1 FFGLM 5
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Db        1 FFGLM 5


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Matches    5;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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US-10-805-881-1
;   Sequence 1, Application US/10805881
;   Publication No. US20040171093A1
;   GENERAL INFORMATION:
;   APPLICANT: Wells, Ibert C.
;   TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound
;   TITLE OF INVENTION: Magnesium for Disease Diagnosis
;   FILE REFERENCE: 800812-0005
;   CURRENT APPLICATION NUMBER: US/10/805,881
;   CURRENT FILING DATE: 2004-03-22
;   PRIOR APPLICATION NUMBER: US 10/053,669
;   PRIOR FILING DATE: 2002-01-24
;   PRIOR APPLICATION NUMBER: US 10/695,536
;   PRIOR FILING DATE: 2003-10-28
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: Patentin version 3.2
;   SEQ ID NO 1
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;     NAME/KEY: MOD_RES
;     LOCATION: (5)..(5)
;     OTHER INFORMATION: AMIDATION
US-10-805-881-1

Qy        1 FFGLM 5
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Db        1 FFGLM 5


Query Match           100.0%;    Score 27;  DB 4;  Length 5;
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RESULT 6
US-10-720-039-3
;   Sequence 3, Application US/10720039
;   Publication No. US20040025786A1
;   GENERAL INFORMATION:
;   APPLICANT: Kream, Richard M.
;   APPLICANT: Kream, Richard M.
;   APPLICANT: Kream, Richard M.
;   TITLE OF INVENTION: Method Of Transporting A Chimeric Hybrid Molecule Across The Bloo
;   TITLE OF INVENTION: Barrier
;   FILE REFERENCE: Kream
;   CURRENT APPLICATION NUMBER: US/10/720,039
;   CURRENT FILING DATE: 2003-11-20
;   NUMBER OF SEQ ID NOS: 3
;   SOFTWARE: Patentin version 3.1
;   SEQ ID NO 3
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: mammalian
US-10-720-039-3

Qy        1 FFGLM 5
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Db        1 FFGLM 5


Query Match           100.0%;    Score 27;  DB 5;  Length 5;
Best Local Similarity 100.0%;    Pred. No. 1.7e+06;
Matches    5;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;


RESULT 7
US-10-497-628-15
;   Sequence 15, Application US/10497628
;   Publication No. US20050009752A1
;   GENERAL INFORMATION:
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OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: November 26, 2005, 02:17:59 ; Search time 8 Seconds
(without alignments)
1.894 Million cell updates/sec

Title: US-10-805-881-1
Perfect score: 27
Sequence: 1 FFGLM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 220

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	12	44.4	4	7	US-11-064-785-1	Sequence 1, Appli
2	12	44.4	4	7	US-11-016-706-52	Sequence 52, Appl
3	12	44.4	5	7	US-11-021-441-62	Sequence 62, Appl
4	10	37.0	4	7	US-11-046-456-27	Sequence 27, Appl
5	10	37.0	4	7	US-11-046-644-27	Sequence 27, Appl
6	10	37.0	4	7	US-11-052-168A-38	Sequence 38, Appl
7	10	37.0	4	7	US-11-052-145-32	Sequence 32, Appl
8	10	37.0	4	5	US-10-502-145-32	Sequence 32, Appl
9	10	33.3	5	1	US-10-726-554-12	Sequence 12, Appl
10	9	33.3	5	7	US-10-997-066-17	Sequence 17, Appl
11	9	33.3	5	7	US-11-035-682-13	Sequence 13, Appl
12	9	33.3	5	7	US-11-079-969-2	Sequence 2, Appl
13	9	33.3	5	7	US-11-054-515-3167	Sequence 3167, Ap
14	9	25.9	5	7	US-11-187-989-7	Sequence 7, Appli
15	9	25.9	4	7	US-10-977-367-21	Sequence 21, Appl
16	9	25.9	4	1	US-10-997-066-16	Sequence 16, Appl
17	9	25.9	4	1	US-10-966-648-28	Sequence 28, Appl
18	9	25.9	4	7	US-11-035-682-12	Sequence 12, Appl
19	7	25.9	4	7	US-11-113-224-57	Sequence 57, Appl
20	7	25.9	4	7	US-11-113-224-59	Sequence 59, Appl
21	7	25.9	4	7	US-10-977-367-22	Sequence 22, Appl
22	7	25.9	5	7	US-10-977-367-24	Sequence 24, Appl
23	7	25.9	5	1	US-10-977-367-37	Sequence 37, Appl
24	7	25.9	5	1	US-10-990-627-10	Sequence 10, Appl
25	7	25.9	5	7	US-11-053-100-4	Sequence 4, Appli
26	7	25.9	5	7	US-11-053-100-5	Sequence 5, Appli
27	7	25.9	5	1	US-11-053-100-6	Sequence 6, Appli
28	7	25.9	5	7	US-11-054-515-2210	Sequence 2210, Ap
29	7	25.9	5	7	US-11-054-515-3174	Sequence 3174, Ap
30	6	22.2	5	7	US-11-052-168A-4	Sequence 4, Appli
31	6	22.2	3	7	US-11-052-168A-39	Sequence 39, Appl
32	6	22.2	3	5	US-10-503-575-48	Sequence 48, Appl
33	6	22.2	4	1	US-10-503-575-49	Sequence 49, Appl
34	6	22.2	4	1	US-10-503-575-59	Sequence 59, Appl
35	6	22.2	4	1	US-10-503-575-62	Sequence 62, Appl
36	6	22.2	4	1	US-10-977-367-1	Sequence 1, Appli
37	6	22.2	4	1	US-10-979-821-77	Sequence 77, Appl
38	6	22.2	4	1	US-10-939-890-262	Sequence 262, App
39	6	22.2	4	1	US-10-939-890-18	Sequence 18, Appl
40	6	22.2	4	1	US-10-939-890-420	Sequence 420, App
41	6	22.2	4	1	US-10-939-890-490	Sequence 490, App
42	6	22.2	4	1	US-10-939-890-791	Sequence 791, App
43	6	22.2	4	1	US-10-939-890-792	Sequence 792, App
44	6	22.2	4	1	US-10-939-890-871	Sequence 871, App

ALIGNMENTS

RESULT 1
US-11-064-785-1
; Sequence 1, Application US/11064785
; Publication No. US20050256030A1
; GENERAL INFORMATION:
; APPLICANT: FENG, BAINIAN
; TITLE OF INVENTION: HETEROCYCLIC SELF-IMMOLATIVE LINKERS AND
; TITLE OF INVENTION: CONJUGATES
; FILE REFERENCE: 39766-0143A
; CURRENT APPLICATION NUMBER: US/11/064,785
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US 60/547,152
; PRIOR FILING DATE: 2004-02-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-064-785-1

Query Match   44.4%; Score 12; DB 7; Length 4;
Best Local Similarity   66.7%; Pred. No. 1.5e+04;
Matches   2; Conservative   0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 FFG 3
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Db   2 FLG 4

RESULT 2
US-11-016-706-52
; Sequence 52, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; FILE REFERENCE: PROTEO.P03CI3
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955

; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 52
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-016-706-52

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Qy          1 FF 2
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Query Match Similarity 44.4%;   Score 12; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
US-11-016-706-52

RESULT 3
US-11-021-441-62
; Sequence 62, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 2821T2003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/615,287
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/599,377
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/23881
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/883,599
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-11-021-441-62

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Db          4 FG 5
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Query Match Similarity 44.4%;   Score 12; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
US-11-021-441-62

RESULT 4
US-11-046-456-27
; Sequence 27, Application US/11046456
; Publication No. US20050256044A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, Bryan
; APPLICANT: Funk, Walter
; APPLICANT: Kakitani, Makoto
; APPLICANT: Oshima, Takeshi
; APPLICANT: Park, Eun Ju
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yagi, Mikio
; APPLICANT: Tomizuka, Kazuma
; TITLE OF INVENTION: Gastrointestinal Proliferative Factor and uses thereof
; FILE REFERENCE: 18824-003001
; CURRENT APPLICATION NUMBER: US/11/046,456
; CURRENT FILING DATE: 2005-01-27
; PRIOR APPLICATION NUMBER: US 60/539,605
; PRIOR FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: US 60/539,605
; PRIOR FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: US 10/488,423
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: PCT/US02/27746
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 27
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-046-456-27

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Query Match Similarity 37.0%;   Score 10; DB 7; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
US-11-046-456-27

RESULT 5
US-11-046-644-27
; Sequence 27, Application US/11046644
; Publication No. US20050256036A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, Bryan
; APPLICANT: Funk, Walter
; APPLICANT: Kakitani, Makoto
; APPLICANT: Oshima, Takeshi
; APPLICANT: Park, Emily
; APPLICANT: Tang, Y. Tom
; APPLICANT: Tomizuka, Kazuma
; APPLICANT: Yagi, Mikio
; TITLE OF INVENTION: Gastrointestinal proliferative factor and uses thereof
; FILE REFERENCE: 11926-194001
; CURRENT APPLICATION NUMBER: US/11/046,644
; CURRENT FILING DATE: 2005-01-27
; PRIOR APPLICATION NUMBER: US 60/539,605
; PRIOR FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: US 60/619,241
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 27
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-046-644-27

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Qy          3 GLM 5
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Query Match Similarity 37.0%;   Score 10; DB 7; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OM protein - protein search, using sw model

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Run on: November 26, 2005, 03:02:43 ; Search time 60.2857 Seconds
(without alignments)
29.153 Million cell updates/sec

Title: US-10-805-881-2
Perfect score: 21
Sequence: 1 FGLM 4
Scoring table: BLOSUM62
Searched: Gapop 10.0 , Gapext 0.5
                2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 990051

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : A.Geneseq_21:*
            1: geneseqp1980s:*
            2: geneseqp1990s:*
            3: geneseqp2000s:*
            4: geneseqp2001s:*
            5: geneseqp2002s:*
            6: geneseqp2003as:*
            7: geneseqp2003bs:*
            8: geneseqp2004s:*
            9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB	ID	Description
1	21	100.0	4	2	AAW41683	Aaw41683 Peptide u
2	21	100.0	4	2	AAY31075	Aay31075 Non-cross
3	21	100.0	4	3	AAB23026	Aab23026 Human/rat
4	21	100.0	4	4	AAY67577	Aay67577 P antagon
5	21	100.0	4	4	AAB91447	Aab91447 Tachykini
6	21	100.0	4	5	ABB10091	Abb10091 Substance
7	21	100.0	4	5	AAU77846	Aau77846 Tachykini
8	21	100.0	4	7	ADE94198	Ade94198 High acti
9	21	100.0	4	8	ADR43772	Adr43772 Human mag
10	21	100.0	5	7	AAR33009	Aar33009 Alpha-sub
11	21	100.0	5	7	AAR33008	Aar33008 Alpha-sub
12	21	100.0	5	7	AAR33007	Aar33007 Alpha-sub
13	21	100.0	5	7	AAR33010	Aar33010 Alpha-sub
14	21	100.0	5	7	AAR54549	Aar54549 Cholecyst
15	21	100.0	5	2	AAR54551	Aar54551 Cholecyst
16	21	100.0	5	2	AAR54550	Aar54550 Cholecyst
17	21	100.0	5	2	AAR54548	Aar54548 Cholecyst
18	21	100.0	5	2	AAW41687	Aaw41687 Tetrapept
19	21	100.0	5	2	AAW99643	Aaw99643 Substance
20	21	100.0	5	2	AAY50325	Aay50325 Neutrophi
21	21	100.0	5	2	AAW92660	Aaw92660 Human tac
22	21	100.0	5	2	AAW92702	Aaw92702 Human tac
23	21	100.0	5	3	AAB23025	Aab23025 Human/rat
24	21	100.0	5	3	AAY67576	Aay67576 P antagon
25	21	100.0	5	4	AAB91428	Aab91428 Tachykini
26	21	100.0	5	4	AAB91389	Aab91389 Tachykini
27	21	100.0	5	5	ABB10090	Abb10090 Substance
28	21	100.0	5	5	ABB10089	Abb10089 Substance
29	21	100.0	5	5	ABB10088	Abb10088 Substance
30	21	100.0	5	5	AAU77845	Aau77845 Tachykini
31	21	100.0	5	7	ADE94205	Ade94205 High acti
32	21	100.0	5	7	ADE94203	Ade94203 High acti
33	21	100.0	5	7	ADE94204	Ade94204 High acti
34	21	100.0	5	7	ADN95078	Adn95078 Mammalian
35	21	100.0	5	8	ADF92530	Adf92530 Mammalian
36	21	100.0	5	8	ADR03603	Adr03603 E. colii m
37	21	100.0	5	8	ADR43771	Adr43771 Human mag
38	21	100.0	5	9	ADV44808	Adv44808 Sequence
39	21	100.0	6	1	AAP40519	Aap40519 Sequence
40	21	100.0	6	1	AAP50694	Aap50694 Sequence
41	21	100.0	6	1	AAP50632	Aap50632 Substance
42	21	100.0	6	1	AAP61486	Aap61486 Peptide h
43	21	100.0	6	1	AAR07893	Aar07893 Cyclopept
44	21	100.0	6	2	AAR07899	Aar07899 Cyclopept
45	21	100.0	6	2	AAR21959	Aar21959 Substance

ALIGNMENTS

RESULT 1
AAW41683
ID   AAW41683 standard; peptide; 4 AA.
XX
AC   AAW41683;
XX
DT   09-JUN-1998 (first entry)
XX
DE   Peptide used in ophthalmic drug to treat corneal disorders.
XX
KW   Ophthalmic drug; corneal disorder; ulcer; epithelial peeling; dry eye;
KW   keratitis; insulin like growth factor-I; IGF-I; eye drop.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   Modified-site   4
FT   /note= "C-terminal amide"
XX
PN   WO9749419-A1.
XX
PD   31-DEC-1997.
XX
PF   11-JUN-1997; 97WO-JP002015.
XX
PR   26-JUN-1996; 96JP-00165612.
XX
PA   (SANT) SANTEN PHARM CO LTD.
XX
PI   Nishida T, Nakamura M, Nakata K;
XX
DR   WPI; 1998-076907/07.
XX
PT   Ophthalmic drug composition containing tetra:peptide - is useful as
PT   corneal disorder remedy for corneal ulcer, corneal epithelial peeling,
PT   dry eye, keratitis.
XX
PS   Claim 1; Page 15; 19pp; Japanese.
XX
CC   The present sequence represents a tetrapeptide which is the active
CC   ingredient in an ophthalmic drug composition. It is used, together with
CC   insulin like growth factor-I (IGF-I), to treat corneal disorders such as
CC   corneal ulcer, corneal epithelial peeling, dry eye and keratitis. The
CC   dosage is 0.1-5000 (preferably 1-1000) mg/day of the tetrapeptide and
CC   0.001-100 (preferably 0.01-10) mg/day of IGF-I. The preferable form of
CC   the composition is eye drops.

SQ   Sequence 4 AA;

      Query Match   100.0%;   Score 21; DB 2;   Length 4;
      Best Local Similarity 100.0%;   Pred. No. 2e+06;
Matches   4; Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 FGLM 4
        ||||
Db   1 FGLM 4

RESULT 2
ID   AAY31075 standard; peptide; 4 AA.
XX
AC   AAY31075;
XX
DT   21-OCT-1999 (first entry)
XX
DE   Non-crosslinked protein particle peptide 124.
XX
KW   Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
KW   albumin; haemoglobin; nanometer; micrometer; clearance.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   Modified-site 4
FT   /note= "C-terminal amide"
XX
PN   US5945033-A.
XX
PD   31-AUG-1999.
XX
PF   12-NOV-1996;   96US-00747137.
XX
PR   15-JAN-1991;   91US-00641720.
PR   13-OCT-1992;   92US-00959560.
PR   01-JUN-1993;   93US-00069831.
PR   14-MAR-1994;   94US-00212546.
XX
PA   (HEMO-) HEMOSPHERE INC.
XX
PI   Yen RCK;
XX
DR   WPI; 1999-508153/42.
XX
PT   Non-crosslinked protein particles for therapeutic and diagnostic use.
XX
PS   Example 22; Col 103-104; 65pp; English.
XX
CC   This invention describes a novel aqueous suspension of monodisperse
CC   particles on non-crosslinked, non-denatured albumin (50-5000 nm) which is
CC   stable against dissolving upon dilution with an alcohol-free aqueous
CC   medium. The method involves (a) forming an aqueous solution containing
CC   albumin and hemoglobin and (b) treating the aqueous solution with an
CC   alcohol to cause the solution to become turbid. The particles are useful
CC   as agents for in vivo administration, either of their own administration
CC   or as a vehicle for other therapeutic or diagnostic agents. The method
CC   permits the formation of albumin and hemoglobin particles in the
CC   nanometer and micrometer size range, in a form closer to their natural
CC   form than the forms of the prior art. The particles therefore constitute
CC   a more closely controlled agent for in vivo administration, with greater
CC   ease of clearance from the body after their period of usefulness.
CC   AAY30952-Y31135 represent peptides used in the method of the invention
XX
SQ   Sequence 4 AA;

      Query Match   100.0%;   Score 21; DB 2;   Length 4;
      Best Local Similarity 100.0%;   Pred. No. 2e+06;
Matches   4; Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 FGLM 4
        ||||
Db   1 FGLM 4

Db   1 FGLM 4

RESULT 3
ID   AAB23026 standard; peptide; 4 AA.
XX
AC   AAB23026;
XX
DT   16-JAN-2001 (first entry)
XX
DE   Human/rat tachykinin Substance P C-terminal tetrapeptide.
XX
KW   Substance P; tachykinin; human; rat; magnesium binding defect;
KW   sodium sensitive essential hypertension; insulin resistance;
KW   type 2 diabetes; antibody; immunoassay; quantification.
XX
OS   Homo sapiens.
OS   Rattus sp.
XX
FH   Key   Location/Qualifiers
FT   Modified-site 4
FT   /note= "C-terminal amide"
XX
PN   WO200054053-A1.
XX
PD   14-SEP-2000.
XX
PF   09-MAR-2000;   2000WO-US003707.
XX
PR   10-MAR-1999;   99US-00265690.
XX
PA   (WELL/) WELLS I C.
XX
PI   Wells IC;
XX
DR   WPI; 2000-587457/55.
XX
PT   Detecting magnesium binding defects associated with abnormal
PT   physiological states such as sodium-sensitive essential hypertension and
PT   type 2 insulin-resistant diabetes mellitus, comprises measuring a
PT   specific pentapeptide in blood.
XX
PS   Disclosure; Page 5; 21pp; English.
XX
CC   The inevntion relates to a method for detecting magnesium binding
CC   defects. The method comprises quantitating a tachykinin C-terminal
CC   pentapeptide (e.g., AAB23025) and its degradation products (e.g.,
CC   AAB23026) in blood using an antibody specific for the generalised
CC   mammalian tachykinin C-terminal pentapeptide Phe-(Phe/Val)-Gly-Leu-Met-
CC   NH2 (AAB23028). The method is useful for detecting cellular magnesium
CC   binding defects which are associated with abnormal physiological states
CC   such as sodium-sensitive essential hypertension and type 2 diabetes
CC   mellitus. The present sequence represents the C-terminal 4 amino acids of
CC   the tachykinin Substance P (AAB23027) from human and rat. This is a
CC   degradation product of the Substance P C-terminal pentapeptide (AAB23025)
CC   and may also be assayed according to the method of the invention
XX
SQ   Sequence 4 AA;

      Query Match   100.0%;   Score 21; DB 3;   Length 4;
      Best Local Similarity 100.0%;   Pred. No. 2e+06;
Matches   4; Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 FGLM 4
        ||||
Db   1 FGLM 4

RESULT 4
ID   AAY67577 standard; peptide; 4 AA.

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: November 26, 2005, 03:18:04 ; Search time 16 Seconds
                                              (without alignments)
                                              24.054 Million cell updates/sec

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR.80:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

Title: US-10-805-881-2
Perfect score: 21
Sequence: 1 FGLM 4
Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 6283

Minimum DB seq length: 0
Maximum DB seq length: 30

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	11	1	A60654	substance P - guin
2	21	100.0	11	1	SPHO	substance P - hors
3	21	100.0	11	1	JN0023	substance P - chic
4	21	100.0	11	2	S33300	probable substance
5	21	100.0	11	2	E60409	substance P-like p
6	21	100.0	11	2	F60409	substance P-like p
7	21	100.0	11	2	S23308	substance P - rain
8	21	100.0	19	2	PS0332	phospholipase A2 (
9	21	100.0	10	2	B49581	sialokinin II - ye
10	18	85.7	10	2	B61033	ranatachykinin B -
11	18	85.7	10	2	A49581	sialokinin I - yel
12	18	85.7	10	2	A44867	scyliorhinin I - s
13	18	85.7	11	2	S07203	uperolein - frog (
14	18	85.7	11	2	S07201	physalaemin - frog
15	18	85.7	11	2	A61033	ranatachykinin A -
16	17	81.0	26	2	A34280	phospholipase A2 (
17	17	81.0	27	2	B44180	phospholipase A2 (
18	16	76.2	8	2	D47393	neuropeptide calla
19	16	76.2	10	2	F06527	sperm-activating p
20	16	76.2	10	2	B60589	sperm-activating p
21	16	76.2	12	2	S01749	collagen alpha 1(I
22	16	76.2	12	2	PA0098	ribosomal protein
23	16	76.2	12	2	S07436	tachykinin - Afric
24	16	76.2	16	2	A47393	neuropeptide calla
25	16	76.2	17	2	S50901	chlorophyll a/b-bi
26	16	76.2	18	2	I52651	brain-derived neur
27	16	76.2	18	2	B44995	alkanal monooxygen
28	16	76.2	22	2	A35418	brain natriuretic
29	16	76.2	22	2	JN0910	N4-(beta-N-acetylg
30	16	76.2	27	2	T17067	NADH2 dehydrogenas
31	16	76.2	27	2	S09734	photosystem I prot
32	16	76.2	27	2	S55802	stp protein (Baker
33	16	76.2	27	2	S55801	stp protein (Baker
34	16	76.2	28	2	PQ0691	photosystem I 5.6K
35	16	76.2	28	2	S49924	stp protein (Baker
36	16	76.2	28	2	T06925	hypothetical prote
37	16	76.2	29	2	S07055	photosystem I prot
38	16	76.2	29	2	S08088	gene VII protein -
39	16	76.2	30	2	I83367	intracisternal A p
40	16	76.2	30	2	B44314	gag protein - mous
41	16	76.2	30	2	S02088	blood group Rh-rel
42	16	76.2	30	2	E95079	hypothetical prote
43	16	71.4	5	2	PT0278	Ig heavy chain CRD
44	15	71.4	10	1	SPPGNK	neuromedin K - pig
45	15	71.4	10	2	JN0024	neurokinin A - chi

ALIGNMENTS

RESULT 1
A60654
substance P - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: A60654
R;Murphy, R.
Neuropeptides 14, 105-110, 1989
A;Title: Primary amino acid sequence of guinea-pig substance P.
A;Reference number: A60654; MUID:90044685; PMID:2478925
A;Accession: A60654
A;Molecule type: protein
A;Residues: 1-11 <MUR>
A;Cross-references: UNIPROT:P01290; UNIPARC:UPI000002BD74
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match   100.0%; Score 21; DB 1; Length 11;
Best Local Similarity   100.0%;
Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FGLM 4
              ||||
Db   8 FGLM 11

RESULT 2
SPHO
substance P - horse
C;Species: Equus caballus (domestic horse)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C;Accession: A01558
R;Studer, R.O.; Trzeciak, A.; Lergier, W.
Helv. Chim. Acta 56, 860-866, 1973
A;Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdedarm.
A;Reference number: A01558
A;Accession: A01558
A;Molecule type: protein
A;Residues: 1-11 <STU>
A;Cross-references: UNIPROT:P01290; UNIPARC:UPI000002BD74
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; hormone
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match   100.0%; Score 21; DB 1; Length 11;
Best Local Similarity   100.0%;
Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FGLM 4
              ||||
Db   8 FGLM 11

RESULT 3
JN0023
substance P - chicken
C;Species: Gallus gallus (chicken)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JN0023
R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
Regul. Pept. 20, 171-180, 1988
A;Title: [Arg3]substance P and neurokinin A from chicken small intestine.
A;Reference number: JN0023
A;Accession: JN0023
A;Molecule type: protein
A;Residues: 1-11 <CON>
A;Cross-references: UNIPROT:P19850; UNIPARC:UPI000003S243
A;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match   100.0%; Score 21; DB 2; Length 11;
Best Local Similarity   100.0%; Pred. No. 20;
Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FGLM 4
               ||||
Db   8 FGLM 11

RESULT 4
S33300
probable substance P - smaller spotted catshark
C;Species: Scyliorhinus caniculla (smaller spotted catshark, smaller spotted dogfish)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S33300
R;Waugh, D.; Wang, Y.; Hazon, N.; Balment, R.J.; Conlon, J.M.
Eur. J. Biochem. 214, 469-474, 1993
A;Title: Primary structures and biological activities of substance-P-related peptides fr
A;Reference number: S33300
A;Accession: S33300
A;Molecule type: protein
A;Residues: 1-11 <WAU>
A;Cross-references: UNIPROT:P41333; UNIPARC:UPI000013GFDB
A;Experimental source: brain
C;Function:
C;Description: may play a physiological role in the regulation of cardiovascular and gas
A;Note: substance P is derived by post-translational processing of preprotachykinin A
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match   100.0%; Score 21; DB 2; Length 11;
Best Local Similarity   100.0%; Pred. No. 20;
Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FGLM 4
               ||||
Db   8 FGLM 11

RESULT 5
E60409
substance P-like peptide I - frog (Pseudophryne guentheri)
C;Species: Pseudophryne guentheri
C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 16-Aug-2004
C;Accession: E60409
R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austra
A;Reference number: A60409; MUID:90287814; PMID:2356157
A;Accession: E60409
A;Molecule type: protein
A;Residues: 1-11 <SIM>
A;Cross-references: UNIPROT:P42989; UNIPARC:UPI0000136FD8

C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match   100.0%; Score 21; DB 2; Length 11;
Best Local Similarity   100.0%; Pred. No. 20;
Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FGLM 4
               ||||
Db   8 FGLM 11

RESULT 6
F60409
substance P-like peptide II - frog (Pseudophryne guentheri)
C;Species: Pseudophryne guentheri
C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 16-Aug-2004
C;Accession: F60409
R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austra
A;Reference number: A60409; MUID:90287814; PMID:2356157
A;Accession: F60409
A;Molecule type: protein
A;Residues: 1-11 <SIM>
A;Cross-references: UNIPROT:P42990; UNIPARC:UPI0000136FD9
C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match   100.0%; Score 21; DB 2; Length 11;
Best Local Similarity   100.0%; Pred. No. 20;
Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FGLM 4 .
               ||||
Db   8 FGLM 11

RESULT 7
S23308
substance P - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
C;Accession: S23308
R;Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod
A;Reference number: S23186; MUID:92299992; PMID:1376687
A;Accession: S23308
A;Molecule type: protein
A;Residues: 1-11 <JEN>
A;Cross-references: UNIPROT:P28499; UNIPARC:UPI000003S254
A;Experimental source: brain
C;Function:
C;Description: may play a physiological role in the regulation of cardiovascular and gas
A;Note: substance P is derived by post-translational processing of preprotachykinin A
C;Keywords: neuropeptide; amidated carboxyl end; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match   100.0%; Score 21; DB 2; Length 11;
Best Local Similarity   100.0%; Pred. No. 20;
Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FGLM 4
               ||||
Db   8 FGLM 11

RESULT 8
PS0332
phospholipase A2 (EC 3.1.1.4), sperm - human (fragment)

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: November 26, 2005, 03:17:04 ; Search time 98 Seconds
                 (without alignments)
                 28.797 Million cell updates/sec

Title: US-10-805-881-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 34439

Minimum DB seq length: 0 .
Maximum DB seq length: 30 .

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_05.80:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	Match DB	DB	ID	Description
1	21	100.0	11	11	1	TKN4_PSEGU	P42989 pseudophryn
2	21	100.0	11	11	1	TKN5_PSEGU	P42990 pseudophryn
3	21	100.0	11	11	1	TKNA_CAVPO	P67932 cavia porce
4	21	100.0	11	11	1	TKNA_CHICK	P19850 gallus gall
5	21	100.0	11	11	1	TKNA_HORSE	P67933 equus cabal
6	21	100.0	11	11	1	TKNA_ONCMY	P28499 oncorhynchu
7	21	100.0	11	11	1	TKNA_SCYCA	P41333 scyliorhinu
8	21	100.0	19	11	2	PA2S_HUMAN	P24606 homo sapien
9	21	100.0	19	11	2	Q9S8E2_SPIOL	Q9S8E2 spinacia ol
10	21	100.0	23	11	2	Q4XBU6_PLACH	Q4xbu6 plasmodium
11	21	100.0	27	11	2	Q4SBA4_TETNG	Q4sba4 tetraodon n
12	19	90.5	12	11	2	PA2B_VIPBO	P31859 vipera beru
13	19	90.5	28	11	2	Q9R4Z1_CHLAU	Q9r4z1 chloroflexu
14	18	85.7	10	11	1	TKN1_SCYCA	P08608 scyliorhinu
15	18	85.7	10	11	1	TKNB_RANCA	P22689 rana catesb
16	18	85.7	10	11	1	TKS1_AEDAE	P42634 aedes aegyp
17	18	85.7	10	11	1	TKS2_AEDAE	P42635 aedes aegyp
18	18	85.7	11	11	1	TKN1_UPEIN	P82026 uperoleia i
19	18	85.7	11	11	1	TKN1_UPERU	P08612 uperoleia r
20	18	85.7	11	11	1	TKN2_UPERU	P08616 uperoleia r
21	18	85.7	11	11	1	TKNA_RANCA	P22688 rana catesb
22	18	85.7	11	11	1	TKNA_RANRI	P29207 rana ridibu
23	18	85.7	11	11	1	TKN_PHYFU	P08615 physalaemus
24	18	85.7	14	11	1	TKNM_RANMA	P40951 rana margar
25	18	85.7	15	2	2	Q9UAR8_AEDAE	Q9uar8 aedes aegyp
26	18	85.7	15	2	2	Q9UQA5_HUMAN	Q9uqa5 homo sapien
27	18	85.7	15	2	2	Q8WNQ2_PIG	Q8wnq2 sus scrofa
28	18	85.7	17	2	2	Q7R8B7_PLAYO	Q7r8b7 plasmodium
29	18	85.7	19	2	2	O31045_STRCO	O31045 streptomyce
30	18	85.7	20	2	2	Q6LBT5_BOVIN	Q6lbt5 bos taurus
31	18	85.7	21	2	2	Q61943_MOUSE	Q61943 mus musculu
32	18	85.7	25	2	2	Q80VX3_MOUSE	Q80vx3 mus musculu
33	18	85.7	26	2	2	Q4TDF2_TETNG	Q4tdf2 tetraodon n
34	18	85.7	28	2	2	Q58M67_9CAUD	Q58m67 cyanophage
35	18	85.7	30	2	2	Q4MMZ2_BACCE	Q4mmz2 bacillus ce
36	18	81.0	23	2	2	Q673D7_9CHLR	Q673d7 dehalococco
37	18	81.0	25	2	2	Q90Z49_HAPBU	Q90z49 haplochromi
38	18	81.0	25	2	2	Q99LX4_MOUSE	Q99lx4 mus musculu
39	17	81.0	26	2	2	Q71ZG4_OXYSC	Q71zg4 oxyuranus s
40	17	81.0	26	2	2	Q6IEE1_HUMAN	Q6iee1 homo sapien
41	17	81.0	27	2	2	Q8HKH7_9ACAR	Q8hkh7 aponomma un
42	17	81.0	27	2	2	Q8HKI3_9ACAR	Q8hki3 aponomma co
43	17	81.0	27	2	2	Q56Z51_ARATH	Q56z51 arabidopsis
44	17	81.0	27	2	2	Q71ZG2_OXYSC	Q71zg2 oxyuranus s
45	17	81.0	28	2	2	Q673D9_9CHLR	Q673d9 dehalococco

ALIGNMENTS

RESULT 1
TKN4_PSEGU

ID   TKN4_PSEGU   STANDARD;   PRT;   11 AA.
AC   P42989;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Substance P-like peptide I (PG-SPI).
OS   Pseudophryne guentheri (Guenther's toadlet).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC   Myobatrachinae; Pseudophryne.
OX   NCBI_TaxID=30349;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Skin secretion;
RX   MEDLINE=92087814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;
RA   Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA   Roberts J.D., Melchiorri P., Erspamer V.;
RT   "Six novel tachykinin- and bombesin-related peptides from the skin of
RT   the Australian frog Pseudophryne guentheri.";
RL   Peptides 11:299-304(1990).
-!- FUNCTION: Tachykinins are active peptides which excite neurons,
    evoke behavioral responses, are potent vasodilators and
    secretagogues, and contract (directly or indirectly) many smooth
    muscles.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the skin glands.
-!- SIMILARITY: Belongs to the tachykinin family.

This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

DR   PIR; E60409; E60409.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   InterPro; IPR008215; Tachykinin.
DR   Pfam; PF02202; Tachykinin; 1.
DR   SMART; SM00203; TK; 1.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Amidation; Amphibian defense peptide; Direct protein sequencing;
KW   Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.
FT   MOD_RES   1   1   Pyrrolidone carboxylic acid.
FT   MOD_RES   11   11   Methionine amide.
SQ   SEQUENCE   11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Qy   1 FGLM 4
                   ||||

Query Match   100.0%;   Score 21; DB 1; Length 11;
Best Local Similarity 100.0%;   Pred. No. 2.5e+02;
Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 2

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Db       8 FGLM 11

ID   TKN5_PSEGU     STANDARD;      PRT;     11 AA.
AC   P42990;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Substance P-like peptide II (PG-SPII).
OS   Pseudophryne guentheri (Guenther's toadlet).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC   Myobatrachinae; Pseudophryne.
OX   NCBI_TaxID=30349;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Skin secretion;
RX   MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;
RA   Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA   Roberts J.D., Melchiorri P., Erspamer V.;
RT   "Six novel tachykinin- and bombesin-related peptides from the skin of
RT   the Australian frog Pseudophryne guentheri.";
RL   Peptides 11:299-304(1990).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC       evoke behavioral responses, are potent vasodilators and
CC       secretagogues, and contract (directly or indirectly) many smooth
CC       muscles.
CC   -!- TISSUE SPECIFICITY: Expressed by the skin glands.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
CC   -----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   MOD_RES      11     11       Methionine amide.
SQ   SEQUENCE   11 AA;   1293 MW;   3A247C2CC9CB1457 CRC64;
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Qy       1 FGLM 4
           ||||
Db       8 FGLM 11

Query Match   Best Local Similarity   100.0%;   Score 21; DB 1; Length 11;
Matches   4;   Conservative   0;   Mismatches   0;   Pred. No. 2.5e+02;   Indels   0;   Gaps   0;
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RESULT 3

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ID   TKNA_CAVPO     STANDARD;      PRT;     11 AA.
AC   P67932; P01290;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Substance P.
GN   Name=TAC1; Synonyms=NKA, NKNA, TAC2;
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC   Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Small intestine;
RX   MEDLINE=90044685; PubMed=2478925; DOI=10.1016/0143-4179(89)90066-8,
RA   Murphy R.;
RT   "Primary amino acid sequence of guinea-pig substance P.";
RL   Neuropeptides 14:1105-110(1989).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC       evoke behavioral responses, are potent vasodilators and
CC       secretagogues, and contract (directly or indirectly) many smooth
CC       muscles.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
CC   -----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   PIR; A60654; A60654.
DR   InterPro; IPR0020040; Tachy_Neurokinin.
DR   Pfam; PF02202; Tachykinin; 1.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Amidation; Direct protein sequencing; Neuropeptide; Neurotransmitter;
KW   Tachykinin.
FT   MOD_RES      11     11       Methionine amide.
SQ   SEQUENCE   11 AA;   1349 MW;   3E757FB3C9D6C6C7 CRC64;
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```
Qy       1 FGLM 4
           ||||
Db       8 FGLM 11

Query Match   Best Local Similarity   100.0%;   Score 21; DB 1; Length 11;
Matches   4;   Conservative   0;   Mismatches   0;   Pred. No. 2.5e+02;   Indels   0;   Gaps   0;
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RESULT 4

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ID   TKNA_CHICK     STANDARD;      PRT;     11 AA.
AC   P19850;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Substance P.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Intestine;
RX   MEDLINE=88204263; PubMed=2452461; DOI=10.1016/0167-0115(88)90050-X;
RA   Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
RT   "[Arg3]substance P and neurokinin A from chicken small intestine.";
RL   Regul. Pept. 20:171-180(1988).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC       evoke behavioral responses, are potent vasodilators and
CC       secretagogues, and contract (directly or indirectly) many smooth
CC       muscles.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
CC   -----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   PIR; JN0023; JN0023.
DR   InterPro; IPR0020040; Tachy_Neurokinin.
DR   Pfam; PF02202; Tachykinin; 1.
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OM protein - protein search, using sw model

Copyright (c) 1993 - 2005 Compugen Ltd.
GenCore version 5.1.6

Run on: November 26, 2005, 03:06:43 ; Search time 16 Seconds
(without alignments)
20.669 Million cell updates/sec

Title: US-10-805-881-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 265581

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptcdata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptcdata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptcdata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptcdata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptcdata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB ID	Description
1	21	100.0	4	US-08-441-591-63	Sequence 63, Appl
2	21	100.0	4	US-08-303-362A-63	Sequence 63, Appl
3	21	100.0	4	US-09-265-690C-2	Sequence 2, Appli
4	21	100.0	4	US-09-635-266-3	Sequence 3, Appli
5	21	100.0	4	US-10-230-133-3	Sequence 3, Appli
6	21	100.0	2	US-09-623-548A-623	Sequence 623, Appli
7	21	100.0	2	US-09-657-276-623	Sequence 623, App
8	21	100.0	4	US-10-695-536-3	Sequence 3, Appli
9	21	100.0	4	US-09-657-276-623	Sequence 623, App
10	21	100.0	4	PCT-US95-05600-80	Sequence 80, Appl
11	21	100.0	4	US-07-934-553-2	Sequence 2, Appli
12	21	100.0	2	US-08-225-474-2	Sequence 2, Appli
13	21	100.0	1	US-08-070-301-6	Sequence 6, Appli
14	21	100.0	1	US-07-737-371E-6	Sequence 6, Appli
15	21	100.0	1	US-07-737-371E-48	Sequence 48, Appli
16	21	100.0	2	US-09-265-690C-1	Sequence 1, Appli
17	21	100.0	2	US-09-623-548A-604	Sequence 604, App
18	21	100.0	2	US-10-134-187-3	Sequence 3, Appli
19	21	100.0	2	US-09-657-276-565	Sequence 565, App
20	21	100.0	2	US-09-657-276-604	Sequence 604, App
21	21	100.0	2	US-07-934-553-3	Sequence 3, Appli
22	21	100.0	2	US-09-657-276-565	Sequence 565, App
23	21	100.0	1	US-08-225-474-3	Sequence 3, Appli
24	21	100.0	1	US-08-430-238-15	Sequence 15, Appl
25	21	100.0	1	US-07-737-371E-5	Sequence 5, Appli
26	21	100.0	2	US-09-317-125-5	Sequence 5, Appli
27	21	100.0	2	US-09-428-692-41	Sequence 41, Appl
28	21	100.0	6 2	US-09-623-548A-566	Sequence 566, App
29	21	100.0	6 2	US-09-623-548A-595	Sequence 595, App
30	21	100.0	6 2	US-09-623-548A-597	Sequence 597, App
31	21	100.0	6 2	US-09-623-548A-601	Sequence 601, App
32	21	100.0	6 2	US-09-623-548A-8	Sequence 8, Appl
33	21	100.0	6 2	US-09-623-548A-42	Sequence 42, Appl
34	21	100.0	6 2	US-09-623-548A-596	Sequence 596, App
35	21	100.0	6 2	US-09-623-548A-607	Sequence 607, App
36	21	100.0	7 2	US-07-712-828B-7	Sequence 7, Appl
37	21	100.0	7 1	US-09-657-276-601	Sequence 601, App
38	21	100.0	7 2	US-09-623-548A-596	Sequence 596, App
39	21	100.0	7 2	US-09-623-548A-607	Sequence 607, App
40	21	100.0	7 2	US-09-428-692-42	Sequence 42, Appl
41	21	100.0	7 2	US-10-134-187-2	Sequence 2, Appli
42	21	100.0	7 2	US-09-657-276-596	Sequence 596, App
43	21	100.0	7 2	US-09-657-276-607	Sequence 607, App
44	21	100.0	8 1	US-07-737-371E-10	Sequence 10, Appl
45	21	100.0	8 1	US-07-737-371E-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1
US-08-441-591-63
Sequence 63, Application US/08441591
Patent No. 5637682

GENERAL INFORMATION:
; APPLICANT: NIEUWLANDT, D.; GOLD, L. AND WECKER, M.
; TITLE OF INVENTION: HIGH-AFFINITY
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
; TITLE OF INVENTION: TO THE TACHYKININ
; TITLE OF INVENTION: SUBSTANCE P
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,591
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/303,362
; FILING DATE: 9-SEPTEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 8-SEPTEMBER 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NBX21/C
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-441-591-63

Qy   1 FGLM 4
       ||||
Db   1 FGLM 4

Query Match   100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-08-303-362A-63

RESULT 2
US-08-303-362A-63
Sequence 63, Application US/0830336362A
Patent No. 5648214
GENERAL INFORMATION:
APPLICANT: NIEUWLANDT, D.; GOLD, L. AND WECKER, M.
TITLE OF INVENTION: HIGH-AFFINITY
TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
TITLE OF INVENTION: TO THE TACHYKININ
TITLE OF INVENTION: SUBSTANCE P
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,362A
FILING DATE: 9-SEPTEMBER-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 4
TYPE: amino acid
STRANDEDNESS: single

; TOPOLOGY: linear
US-08-303-362A-63

Qy   1 FGLM 4
       ||||
Db   1 FGLM 4

Query Match   100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-265-690C-2

RESULT 3
US-09-265-690C-2
Sequence 2, Application US/09265690C
Patent No. 6372440
GENERAL INFORMATION:
APPLICANT: Wells, Ibert
TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mag
FILE REFERENCE: 1427001
CURRENT APPLICATION NUMBER: US/09/265,690C
CURRENT FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: AMIDATION
US-09-265-690C-2

; TOPOLOGY: linear
US-09-265-690C

Qy   1 FGLM 4
       ||||
Db   1 FGLM 4

Query Match   100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-635-266-3

RESULT 4
US-09-635-266-3
Sequence 3, Application US/09635266
Patent No. 6455734
GENERAL INFORMATION:
APPLICANT: Wells, Ibert
TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
TITLE OF INVENTION: methods for treatment of abnormal physiological states
FILE REFERENCE: N1427-002
CURRENT APPLICATION NUMBER: US/09/635,266
CURRENT FILING DATE: 2000-08-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: AMIDATION
US-09-635-266-3

Qy   1 FGLM 4
       ||||

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: November 26, 2005, 03:13:24 ; Search time 46 Seconds
(without alignments)
36.333 Million cell updates/sec

Title: US-10-805-881-2
Perfect score: 21
Sequence: 1 FGLM 4
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 439079

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	21	100.0	4	4	US-10-230-133-3	Sequence 3, Appli
3	21	100.0	4	4	US-10-053-669-2	Sequence 2, Appli
4	21	100.0	4	5	US-10-695-536-3	Sequence 3, Appli
5	21	100.0	4	4	US-10-805-881-2	Sequence 2, Appli
6	21	100.0	5	2	US-10-497-628-2	Sequence 2, Appli
7	21	100.0	4	6	US-11-018-690-3	Sequence 3, Appli
8	21	100.0	4	6	US-11-066-697-623	Sequence 623, App
9	21	100.0	4	3	US-09-265-690C-1	Sequence 1, Appli
10	21	100.0	3	4	US-10-053-669-1	Sequence 1, Appli
11	21	100.0	5	4	US-10-134-187-3	Sequence 3, Appli
12	21	100.0	5	4	US-10-497-628-17	Sequence 17, Appl
13	21	100.0	5	4	US-10-688-741-3	Sequence 3, Appl
14	21	100.0	4	4	US-10-346-737A-30	Sequence 30, Appl
15	21	100.0	5	1	US-10-720-039-3	Sequence 3, Appli
16	21	100.0	5	4	US-10-497-628-15	Sequence 15, Appl
17	21	100.0	5	4	US-10-497-628-16	Sequence 16, Appl
18	21	100.0	5	6	US-11-066-697-565	Sequence 565, App
19	21	100.0	5	6	US-11-066-697-604	Sequence 604, App
20	21	100.0	6	4	US-10-497-628-14	Sequence 14, Appl
21	21	100.0	6	4	US-10-168-789A-38	Sequence 38, Appli
22	21	100.0	6	4	US-10-025-494-3	Sequence 3, Appli
23	21	100.0	5	4	US-10-497-628-14	Sequence 14, Appl
24	21	100.0	5	4	US-10-776-330-4	Sequence 4, Appli
25	21	100.0	6	6	US-11-066-697-566	Sequence 566, App
26	21	100.0	6	6	US-11-066-697-595	Sequence 595, App
27	21	100.0	6	6	US-11-066-697-597	Sequence 597, App
28	21	100.0	6	6	US-11-066-697-601	Sequence 601, App
29	21	100.0	6	4	US-10-036-542-110	Sequence 110, App
30	21	100.0	7	4	US-10-036-542-111	Sequence 111, App
31	21	100.0	7	4	US-10-168-789A-37	Sequence 37, Appl
32	21	100.0	7	4	US-10-134-187-2	Sequence 2, Appli
33	21	100.0	7	4	US-10-688-741-2	Sequence 2, Appli
34	21	100.0	7	1	US-10-720-039-2	Sequence 2, Appli
35	21	100.0	7	4	US-10-497-628-13	Sequence 13, Appl
36	21	100.0	7	6	US-11-066-697-596	Sequence 596, App
37	21	100.0	7	6	US-11-066-697-607	Sequence 607, App
38	21	100.0	6	4	US-10-168-789A-36	Sequence 36, Appl
39	21	100.0	6	4	US-11-025-494-2	Sequence 2, Appli
40	21	100.0	5	4	US-11-066-697-592	Sequence 592, App
41	21	100.0	6	6	US-11-066-697-583	Sequence 583, App
42	21	100.0	6	6	US-11-066-697-600	Sequence 600, App
43	21	100.0	5	6	US-10-036-542-112	Sequence 112, App
44	21	100.0	5	6	US-11-066-697-595	Sequence 595, App
45	21	100.0	4	4	US-10-168-789A-35	Sequence 35, Appl

ALIGNMENTS

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US-09-265-690C-2

Sequence 2, Application US/09265690C
; Publication No. US20010053345A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
; TITLE OF INVENTION: for Disease Diagnosis
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265,690C
; CURRENT FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.0
;
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)-.(4)
; OTHER INFORMATION: AMIDATION
US-09-265-690C-2

Query Match   100.0%; Score 21; DB 3; Length 4;
Best Local Similarity   100.0%; Pred. No. 1.7e+06;
Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db    1  FGLM  4
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RESULT 2
US-10-230-133-3
; Sequence 3, Application US/10230133
; Publication No. US20030040625A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
; TITLE OF INVENTION: methods for treatment of abnormal physiological states
; FILE REFERENCE: 2892-106
; CURRENT APPLICATION NUMBER: US/10/230,133
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 09/635,266
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.0
;
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT

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;     ORGANISM: Homo sapiens
;     FEATURE:
;       NAME/KEY: MOD_RES
;       LOCATION: (4)..(4)
;       OTHER INFORMATION: AMIDATION
US-10-230-133-3

Query Match            100.0%;  Score 21;  DB 4;  Length 4;
Best Local Similarity  100.0%;  Pred. No. 1.7e+06;
Matches  4;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 FGLM 4
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Db    1 FGLM 4


RESULT 3
US-10-053-669-2

;  Sequence 2, Application US/10053669
;  Publication No. US20030077658A1
;  GENERAL INFORMATION:
;     APPLICANT: Wells, Ibert
;     TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
;     TITLE OF INVENTION: for Disease Diagnosis
;     FILE REFERENCE: NI427-005
;     CURRENT APPLICATION NUMBER: US/10/053,669
;     CURRENT FILING DATE: 2002-01-24
;     PRIOR APPLICATION NUMBER: 09/265,690
;     PRIOR FILING DATE: 1999-03-10
;     NUMBER OF SEQ ID NOS: 4
;     SOFTWARE: Patentin version 3.0
;  SEQ ID NO 2
;     LENGTH: 4
;     TYPE: PRT
;     ORGANISM: Homo sapiens
;     FEATURE:
;       NAME/KEY: MOD_RES
;       LOCATION: (4)..(4)
;       OTHER INFORMATION: AMIDATION
US-10-053-669-2

Query Match            100.0%;  Score 21;  DB 4;  Length 4;
Best Local Similarity  100.0%;  Pred. No. 1.7e+06;
Matches  4;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 FGLM 4
        ||||
Db    1 FGLM 4


RESULT 4
US-10-695-536-3

;  Sequence 3, Application US/10695536
;  Publication No. US20040110692A1
;  GENERAL INFORMATION:
;     APPLICANT: Wells, Ibert Clifton
;     TITLE OF INVENTION: Antagonists of the Magnesium Binding Defect as Therapeutic Agents
;     TITLE OF INVENTION: and Methods for Treatment of Abnormal Physiological States
;     FILE REFERENCE: 800812-0008
;     CURRENT APPLICATION NUMBER: US/10/695,536
;     CURRENT FILING DATE: 2003-10-28
;     PRIOR APPLICATION NUMBER: US 10/230,133
;     PRIOR FILING DATE: 2002-08-29
;     PRIOR APPLICATION NUMBER: US 09/635,266
;     PRIOR FILING DATE: 2000-08-09
;     NUMBER OF SEQ ID NOS: 4
;     SOFTWARE: Patentin version 3.2
;  SEQ ID NO 3
;     LENGTH: 4
;     TYPE: PRT
;     ORGANISM: Homo sapiens
;     FEATURE:
;       NAME/KEY: MOD_RES
;       LOCATION: (4)..(4)
;       OTHER INFORMATION: AMIDATION
US-10-695-536-3

Query Match            100.0%;  Score 21;  DB 4;  Length 4;
Best Local Similarity  100.0%;  Pred. No. 1.7e+06;
Matches  4;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 FGLM 4
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Db    1 FGLM 4


RESULT 5
US-10-805-881-2

;  Sequence 2, Application US/10805881
;  Publication No. US20040171093A1
;  GENERAL INFORMATION:
;     APPLICANT: Wells, Ibert C.
;     TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound
;     TITLE OF INVENTION: Magnesium for Disease Diagnosis
;     FILE REFERENCE: 800812-0005
;     CURRENT APPLICATION NUMBER: US/10/805,881
;     CURRENT FILING DATE: 2004-03-22
;     PRIOR APPLICATION NUMBER: US 10/053,669
;     PRIOR FILING DATE: 2002-01-24
;     PRIOR APPLICATION NUMBER: US 10/695,536
;     PRIOR FILING DATE: 2003-10-28
;     NUMBER OF SEQ ID NOS: 4
;     SOFTWARE: Patentin version 3.2
;  SEQ ID NO 2
;     LENGTH: 4
;     TYPE: PRT
;     ORGANISM: Homo sapiens
;     FEATURE:
;       NAME/KEY: MOD_RES
;       LOCATION: (4)..(4)
;       OTHER INFORMATION: AMIDATION
US-10-805-881-2

Query Match            100.0%;  Score 21;  DB 4;  Length 4;
Best Local Similarity  100.0%;  Pred. No. 1.7e+06;
Matches  4;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 FGLM 4
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Db    1 FGLM 4


RESULT 6
US-10-497-628-2

;  Sequence 2, Application US/10497628
;  Publication No. US20050009752A1
;  GENERAL INFORMATION:
;     APPLICANT: Teruo Nishida
;     APPLICANT: Makoto Inui
;     APPLICANT: Masatsugu Nakamura
;     TITLE OF INVENTION: NOVEL PEPTIDE AND PHARMACEUTICAL USE OF THE SAME
;     FILE REFERENCE: 0435S/HG
;     CURRENT APPLICATION NUMBER: US/10/497,628
;     CURRENT FILING DATE: 2004-06-03
;     PRIOR APPLICATION NUMBER: JP 2001-368103
;     PRIOR FILING DATE: 2001-12-01
;     NUMBER OF SEQ ID NOS: 17
;     SOFTWARE: Patentin Ver. 2.1
;  SEQ ID NO 2
;     LENGTH: 4
;     TYPE: PRT
;     ORGANISM: Human
US-10-497-628-2

Query Match            100.0%;  Score 21;  DB 5;  Length 4;
Best Local Similarity  100.0%;  Pred. No. 1.7e+06;
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OM protein - protein search, using sw model

Copyright (c) 1993 - 2005 Compugen Ltd.

GenCore version 5.1.6

Run on: November 26, 2005, 03:09:53 ; Search time 2.85714 Seconds
                                                      (without alignments)
                                                      4.243 Million cell updates/sec

Title: US-10-805-881-2
Perfect score: 21
Sequence: 1 FGLM
Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 7285

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA New:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16	76.2	8	7	US-11-044-051-80	Sequence 80, Appl
2	16	76.2	9	7	US-11-044-051-78	Sequence 78, Appl
3	16	76.2	9	7	US-11-044-051-84	Sequence 84, Appl
4	16	76.2	10	7	US-11-044-051-77	Sequence 77, Appl
5	16	76.2	10	7	US-11-044-051-85	Sequence 85, App
6	16	76.2	10	7	US-11-044-051-87	Sequence 87, Appl
7	16	76.2	13	7	US-11-044-051-88	Sequence 88, Appl
8	16	76.2	13	7	US-10-986-501-361	Sequence 361, Appl
9	16	76.2	16	7	US-11-044-051-81	Sequence 81, Appl
10	16	76.2	19	7	US-10-503-575-149	Sequence 149, App
11	16	76.2	19	7	US-10-503-575-2170	Sequence 2170, Ap
12	16	76.2	8	7	US-11-054-515-3132	Sequence 3132, Ap
13	15	71.4	12	7	US-10-923-805-4	Sequence 4, Appli
14	15	71.4	12	7	US-10-511-559-478	Sequence 478, App
15	15	71.4	13	7	US-10-511-559-479	Sequence 479, App
16	15	71.4	13	7	US-10-511-559-480	Sequence 480, App
17	15	71.4	13	7	US-10-511-559-481	Sequence 481, App
18	15	71.4	13	7	US-10-511-559-482	Sequence 482, App
19	15	71.4	13	7	US-10-511-559-2943	Sequence 2943, Ap
20	15	71.4	15	7	US-10-515-515-259	Sequence 259, App
21	15	71.4	15	7	US-10-503-575-50	Sequence 50, Appl
22	15	71.4	19	7	US-11-021-441-177	Sequence 177, Appl
23	15	71.4	28	7	US-10-986-501-10	Sequence 10, Appl
24	14	66.7	30	7	US-11-032-498-82	Sequence 82, Appl
25	14	66.7	10	7	US-11-044-051-82	Sequence 82, Ap
26	14	66.7	10	7	US-11-044-051-83	Sequence 83, Appl
27	14	66.7	10	7	US-11-044-051-86	Sequence 86, Appl
28	14	66.7	10	7	US-11-044-051-86	Sequence 86, Appl
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30	14	66.7	13	7	US-11-054-515-2976	Sequence 2976, Ap
31	14	66.7	15	7	US-11-054-515-3004	Sequence 3004, Ap
32	14	66.7	16	7	US-11-054-515-3071	Sequence 3071, Ap
33	14	66.7	17	7	US-11-054-515-2929	Sequence 2929, Ap
34	14	66.7	18	7	US-11-119-581-53	Sequence 53, Appl
35	14	66.7	18	7	US-11-054-515-3136	Sequence 3136, Ap
36	14	66.7	26	7	US-10-939-890-484	Sequence 484, Appl
37	14	66.7	1	7	US-10-494-781-21	Sequence 21, Appl
38	13	61.9	7	7	US-11-053-100-9	Sequence 9, Appli
39	13	61.9	9	7	US-11-054-515-2178	Sequence 2178, Ap
40	13	61.9	10	7	US-11-152-747-40	Sequence 40, Appl
41	13	61.9	10	7	US-11-054-515-2957	Sequence 2957, Ap
42	13	61.9	12	7	US-10-983-464-18	Sequence 18, Appl
43	13	61.9	1	7	US-11-054-515-3176	Sequence 3176, Appl
44	14	66.7	14	7	US-10-939-890-86	Sequence 86, Appl
45	13	61.9	14	7	US-11-054-515-2462	Sequence 2462, Ap

ALIGNMENTS

RESULT 1
US-11-044-051-80
; Sequence 80, Application US/11044051
; Publication No. US20050255553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, Danisle
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459,263
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 80
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-044-051-80

Query Match   76.2%; Score 16; DB 7; Length 8;
Best Local Similarity   100.0%; Pred. No. 1.5e+04;
Matches   3; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FGL 3
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Db   3 FGL 5

RESULT 2
US-11-044-051-78
; Sequence 78, Application US/11044051
; Publication No. US20050255553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, Danisle
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459,263

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;  PRIOR FILING DATE: 2004-02-09
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: Patentin version 3.2
;  SEQ ID NO 78
;  LENGTH: 9
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-11-044-051-78

Qy  Query Match
Db  Best Local Similarity  100.0%;  Score 16;  DB 7;  Length 9;
    Matches  3;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy       1  FGL  3
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Db       2  FGL  4


RESULT 3
US-11-044-051-79
;  Sequence 79, Application US/11044051
;  Publication No. US20050255553A1
;  GENERAL INFORMATION:
;  APPLICANT: VAN PEL, Aline
;  APPLICANT: GODELAINE, Danièle
;  APPLICANT: CARRASCO, Javier
;  APPLICANT: BRASSEUR, Francis
;  APPLICANT: BOON-FALLEUR, Thierry
;  TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
;  FILE REFERENCE: LUD 5888 US
;  CURRENT APPLICATION NUMBER: US/11/044,051
;  CURRENT FILING DATE: 2005-01-28
;  PRIOR APPLICATION NUMBER: US 60/459,263
;  PRIOR FILING DATE: 2004-02-09
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: Patentin version 3.2
;  SEQ ID NO 79
;  LENGTH: 9
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-11-044-051-79

Qy  Query Match
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Qy       1  FGL  3
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Db       3  FGL  5


RESULT 4
US-11-044-051-77
;  Sequence 77, Application US/11044051
;  Publication No. US20050255553A1
;  GENERAL INFORMATION:
;  APPLICANT: VAN PEL, Aline
;  APPLICANT: GODELAINE, Danièle
;  APPLICANT: CARRASCO, Javier
;  APPLICANT: BRASSEUR, Francis
;  APPLICANT: BOON-FALLEUR, Thierry
;  TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
;  FILE REFERENCE: LUD 5888 US
;  CURRENT APPLICATION NUMBER: US/11/044,051
;  CURRENT FILING DATE: 2005-01-28
;  PRIOR APPLICATION NUMBER: US 60/459,263
;  PRIOR FILING DATE: 2004-02-09
;  NUMBER OF SEQ ID NOS: 111
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Qy       1  FGL  3
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Db       3  FGL  5


RESULT 5
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;  Sequence 85, Application US/11044051
;  Publication No. US20050255553A1
;  GENERAL INFORMATION:
;  APPLICANT: VAN PEL, Aline
;  APPLICANT: GODELAINE, Danièle
;  APPLICANT: CARRASCO, Javier
;  APPLICANT: BRASSEUR, Francis
;  APPLICANT: BOON-FALLEUR, Thierry
;  TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
;  FILE REFERENCE: LUD 5888 US
;  CURRENT APPLICATION NUMBER: US/11/044,051
;  CURRENT FILING DATE: 2005-01-28
;  PRIOR APPLICATION NUMBER: US 60/459,263
;  PRIOR FILING DATE: 2004-02-09
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: Patentin version 3.2
;  SEQ ID NO 85
;  LENGTH: 10
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-11-044-051-85

Qy  Query Match
Db  Best Local Similarity  76.2%;  Score 16;  DB 7;  Length 10;
    Matches  3;  Conservative  0;  Pred. No. 16;  Mismatches  0;  Indels  0;  Gaps  0;

Qy       1  FGL  3
            |||
Db       3  FGL  5


RESULT 6
US-11-044-051-87
;  Sequence 87, Application US/11044051
;  Publication No. US20050255553A1
;  GENERAL INFORMATION:
;  APPLICANT: VAN PEL, Aline
;  APPLICANT: GODELAINE, Danièle
;  APPLICANT: CARRASCO, Javier
;  APPLICANT: BRASSEUR, Francis
;  APPLICANT: BOON-FALLEUR, Thierry
;  TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
;  FILE REFERENCE: LUD 5888 US
;  CURRENT APPLICATION NUMBER: US/11/044,051
;  CURRENT FILING DATE: 2005-01-28
;  PRIOR APPLICATION NUMBER: US 60/459,263
;  PRIOR FILING DATE: 2004-02-09
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: Patentin version 3.2
;  SEQ ID NO 87
;  LENGTH: 10
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-11-044-051-87

Qy  Query Match
Db  Best Local Similarity  76.2%;  Score 16;  DB 7;  Length 10;
    Matches  3;  Conservative  0;  Pred. No. 16;  Mismatches  0;  Indels  0;  Gaps  0;

Qy       1  FGL  3
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OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: November 26, 2005, 02:18:39 ; Search time 182 Seconds
                                             (without alignments)
                                             9.657 Million cell updates/sec

Title: US-10-805-881-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
                    Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 25265

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_21:*
                    1: geneseqp1980s:*
                    2: geneseqp1990s:*
                    3: geneseqp2000s:*
                    4: geneseqp2001s:*
                    5: geneseqp2002s:*
                    6: geneseqp2003as:*
                    7: geneseqp2003bs:*
                    8: geneseqp2004s:*
                    9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%Query Match	Length	DB ID	Description
1	21	100.0	4	2	AAW41683	Aaw41683 Peptide u
2	21	100.0	4	3	AAY31075	Aay31075 Non-cross
3	21	100.0	4	3	AAB23026	Aab23026 Human/rat
4	21	100.0	4	3	AAY67577	Aay67577 P antagon
5	21	100.0	4	4	AAB91447	Aab91447 Tachykini
6	21	100.0	4	5	ABB10091	Abb10091 Substance
7	21	100.0	4	5	AAU77846	Aau77846 Tachykini
8	21	100.0	4	7	ADE94198	Ade94198 High acti
9	21	100.0	4	8	ADR43772	Adr43772 Human mag
10	18	85.7	4	1	AAP61654	Aap61654 Sequence
11	18	85.7	4	1	AAP71301	Aap71301 Peptide c
12	18	85.7	4	2	AAW41686	Aaw41686 Tetrapept
13	18	85.7	4	5	ABB10092	Abb10092 Substance
14	16	76.2	4	1	AAP61707	Aap61707 Sequence
15	16	76.2	4	1	AAP71312	Aap71312 Peptide c
16	16	76.2	4	2	AAY23485	Aay23485 V beta 6
17	16	76.2	4	3	AAB12293	Aab12293 Prodrug o
18	16	76.2	4	5	AAG62647	Aag62647 Typical t
19	16	76.2	4	6	ABB88046	Abb88046 Enzyme cl
20	16	76.2	4	8	ADL78809	Adl78809 Exemplary
21	16	76.2	4	9	ADY04142	Ady04142 Peptide d
22	15	71.4	3	3	AAY67578	Aay67578 P antagon
23	15	71.4	3	4	AAB91448	Aab91448 Tachykini
24	15	71.4	4	1	AAP60334	Aap60334 Peptide w
25	15	71.4	4	2	AAW77469	Aaw77469 Tetrapept
26	15	71.4	4	2	AAW41684	Aaw41684 Tetrapept
27	15	71.4	4	2	AAW41685	Aaw41685 Tetrapept
28	15	71.4	4	4	AAB91795	Aab91795 Amyloid b
29	15	71.4	4	4	AAB91822	Aab91822 Amyloid b
30	14	66.7	4	1	AAP61659	Aap61659 Sequence
31	14	66.7	4	1	AAP71306	Aap71306 Peptide c
32	14	66.7	4	2	AAR34486	Aar34486 FGIA. 8/1
33	14	66.7	4	2	AAR46020	Aar46020 Serine pr
34	14	66.7	4	2	AAR93149	Aar93149 Mycobacte
35	14	66.7	4	3	AAB12292	Aab12292 Prodrug o
36	14	66.7	4	4	AAB91714	Aab91714 Opioid pe
37	14	66.7	4	5	ABB88045	Abb88045 Enzyme cl
38	14	66.7	4	5	ABG32223	Abg32223 Sheep col
39	14	66.7	4	8	ADQ91509	Adq91509 HIV trunc
40	14	66.7	4	8	ADS74433	Ads74433 Ovine col
41	13	61.9	3	5	ABG77484	Abg77484 Targettin
42	13	61.9	4	1	AAP61658	Aap61658 Sequence
43	13	61.9	4	1	AAP71287	Aap71287 Opiate bi
44	13	61.9	4	1	AAP82691	Aap82691 Renin inh
45	13	61.9	4	2	AAR15768	Aar15768 Farnesyl-

ALIGNMENTS

RESULT 1
AAW41683
ID   AAW41683 standard; peptide; 4 AA.
XX
AC   AAW41683;
XX
DT   09-JUN-1998 (first entry)
XX
DE   Peptide used in ophthalmic drug to treat corneal disorders.
XX
KW   Ophthalmic drug; corneal disorder; ulcer; epithelial peeling; dry eye;
KW   keratitis; insulin like growth factor-I; IGF-I; eye drop.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   Modified-site   4
FT   /note= "C-terminal amide"
XX
PN   WO9749419-A1.
XX
PD   31-DEC-1997.
XX
PF   11-JUN-1997;   97WO-JP002015.
XX
PR   26-JUN-1996;   96JP-00165612.
XX
PA   (SANT) SANTEN PHARM CO LTD.
XX
PI   Nishida T, Nakamura M, Nakata K;
XX
DR   WPI; 1998-076907/07.
XX
PT   Ophthalmic drug composition containing tetra:peptide - is useful as
PT   corneal disorder remedy for corneal ulcer, corneal epithelial peeling,
PT   dry eye, keratitis.
XX
PS   Claim 1; Page 15; 19pp; Japanese.
XX
CC   The present sequence represents a tetrapeptide which is the active
CC   ingredient in an ophthalmic drug composition. It is used, together with
CC   insulin like growth factor-I (IGF-I), to treat corneal disorders such as
CC   corneal ulcer, corneal epithelial peeling, dry eye and keratitis. The
CC   dosage is 0.1-5000 (preferably 1-1000) mg/day of the tetrapeptide and
CC   0.001-100 (preferably 0.01-10) mg/day of IGF-I. The preferable form of
CC   the composition is eye drops
XX

```
SQ    Sequence 4 AA;

      Query Match             100.0%;  Score 21;  DB 2;  Length 4;
      Best Local Similarity   100.0%;  Pred. No. 2e+06;
      Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy              1  FGLM  4
                   ||||
Db              1  FGLM  4


RESULT 2
ID   AAY31075 standard; peptide; 4 AA.
XX
AC   AAY31075;
XX
DT   21-OCT-1999  (first entry)
XX
DE   Non-crosslinked protein particle peptide 124.
XX
KW   Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
KW   albumin; haemoglobin; nanometer; micrometer; clearance.
XX
OS   Synthetic.
XX
FH   Key              Location/Qualifiers
FT   Modified-site    4
FT                    /note= "C-terminal amide"
XX
PN   US5945033-A.
XX
PD   31-AUG-1999.
XX
PF   12-NOV-1996;  96US-00747137.
XX
PR   15-JAN-1991;  91US-00641720.
PR   13-OCT-1992;  92US-00959550.
PR   01-JUN-1993;  93US-00069831.
PR   14-MAR-1994;  94US-00212546.
XX
PA   (HEMO-) HEMOSPHERE INC.
XX
PI   Yen RCK;
XX
DR   WPI; 1999-508153/42.
XX
PT   Non-crosslinked protein particles for therapeutic and diagnostic use.
XX
PS   Example 22; Col 103-104; 65pp; English.
XX
CC   This invention describes a novel aqueous suspension of monodisperse
CC   particles on non-crosslinked, non-denatured albumin (50-5000 nm) which is
CC   stable against dissolving upon dilution with an alcohol-free aqueous
CC   medium. The method involves (a) forming an aqueous solution containing
CC   albumin and hemoglobin and (b) treating the aqueous solution with an
CC   alcohol to cause the solution to become turbid. The particles are useful
CC   as agents for in vivo administration, either of their own administration
CC   or as a vehicle for other therapeutic or diagnostic agents. The method
CC   permits the formation of albumin and hemoglobin particles in the
CC   nanometer and micrometer size range, in a form closer to their natural
CC   form than the forms of the prior art. The particles therefore constitute
CC   a more closely controlled agent for in vivo administration, with greater
CC   ease of clearance from the body after their period of usefulness.
XX
CC   AAY30952-Y31135 represent peptides used in the method of the invention
XX
SQ   Sequence 4 AA;

      Query Match             100.0%;  Score 21;  DB 2;  Length 4;
      Best Local Similarity   100.0%;  Pred. No. 2e+06;
      Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy              1  FGLM  4
                   ||||
Db              1  FGLM  4
```

```
Db              1  FGLM  4
                   ||||

RESULT 3
ID   AAB23026 standard; peptide; 4 AA.
XX
AC   AAB23026;
XX
DT   16-JAN-2001  (first entry)
XX
DE   Human/rat tachykinin Substance P C-terminal tetrapeptide.
XX
KW   Substance P; tachykinin; human; rat; magnesium binding defect;
KW   sodium sensitive essential hypertension; insulin resistance;
KW   type 2 diabetes; antibody; immunoassay; quantification.
XX
OS   Homo sapiens.
OS   Rattus sp.
XX
FH   Key              Location/Qualifiers
FT   Modified-site    4
FT                    /note= "C-terminal amide"
XX
PN   WO200054053-A1.
XX
PD   14-SEP-2000.
XX
PF   09-MAR-2000;  2000WO-US003707.
XX
PR   10-MAR-1999;  99US-00265690.
XX
PA   (WELL/) WELLS I C.
XX
PI   Wells IC;
XX
DR   WPI; 2000-587457/55.
XX
PT   Disclosure; Page 5; 21pp; English.
XX
CC   The invention relates to a method for detecting magnesium binding
CC   defects. The method comprises quantitating a tachykinin C-terminal
CC   pentapeptide (e.g., AAB23025) and its degradation products (e.g.,
CC   AAB23026) in blood using an antibody specific for the generalised
CC   mammalian tachykinin C-terminal pentapeptide Phe-(Phe/Val)-Gly-Leu-Met-
CC   NH2 (AAB23028). The method is useful for detecting cellular magnesium
CC   binding defects which are associated with abnormal physiological states
CC   such as sodium-sensitive essential hypertension and type 2 diabetes
CC   mellitus. The present sequence represents the C-terminal 4 amino acids of
CC   the tachykinin Substance P (AAB23027) from human and rat. This is a
CC   degradation product of the Substance P C-terminal pentapeptide (AAB23025)
CC   and may also be assayed according to the method of the invention
XX
SQ   Sequence 4 AA;

      Query Match             100.0%;  Score 21;  DB 3;  Length 4;
      Best Local Similarity   100.0%;  Pred. No. 2e+06;
      Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy              1  FGLM  4
                   ||||
Db              1  FGLM  4


RESULT 4
ID   AAY67577 standard; peptide; 4 AA.
```

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: November 26, 2005, 02:28:09 ; Search time 38 Seconds
                    (without alignments)
                    10.128 Million cell updates/sec

Title: US-10-805-881-2
Perfect score: 21
Sequence: 1 FGLM 4
Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 86

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : PIR_80:*
            1: piri:*
            2: pir2:*
            3: pir3:*
            4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	10	47.6	4	2	PT0240	Ig heavy chain CRD
2	10	47.6	4	2	A53284	T-cell receptor be
3	8	38.1	4	2	PT0633	T-cell receptor be
4	7	33.3	3	3	B23751	spinal cord peptid
5	7	33.3	4	2	E44823	synaptosomal-assoc
6	7	33.3	4	2	B53284	T-cell receptor be
7	6	28.6	3	3	PT0636	T-cell receptor be
8	6	28.6	4	2	PT0571	T-cell receptor be
9	6	28.6	4	2	A53284	blood cell protein
10	6	28.6	3	3	S68328	growth-modulating
11	6	28.6	3	3	GKHU	bursin - chicken
12	6	28.6	3	3	A60898	spinal cord peptid
13	6	28.6	4	1	A23751	antho-RFamide neur
14	6	28.6	4	2	ECXXA	hypothetical prote
15	6	28.6	4	2	D41654	starvation-induced
16	6	28.6	4	2	S53508	hypothetical prote
17	6	28.6	4	2	T30569	COI intron 16 prot
18	6	28.6	4	2	I38888	autho-RF amide neu
19	6	28.6	4	2	A25844	RPCH-related neuro
20	6	28.6	4	2	A34626	myosin-light-chain
21	6	28.6	4	2	S39390	Ig mu chain V regi
22	6	28.6	4	2	S43959	ubiquitin - rat
23	6	28.6	4	2	S47552	globulin IV alpha
24	6	28.6	4	2	S09478	carbon-monoxide de
25	6	28.6	4	2	PL0140	neuropeptide Antho
26	6	28.6	4	2	JQ1273	neuropeptide Antho
27	6	28.6	4	2	A35779	FMRFamide - polych
28	6	28.6	4	2	A60418	achatin-I - giant
29	6	28.6	4	2	A32480	Ig heavy chain CRD
30	6	28.6	4	2	PT0271	T-cell receptor be
31	6	28.6	4	2	PT0711	T-cell receptor be
32	6	28.6	4	2	PT0698	T-cell receptor be
33	6	28.6	4	2	PT0677	T-cell receptor be
34	6	28.6	4	2	PT0706	T-cell receptor be
35	6	28.6	4	2	PT0675	T-cell receptor be
36	6	28.6	4	2	PT0721	T-cell receptor be
37	6	28.6	4	2	PT0566	T-cell receptor be
38	6	28.6	4	2	ECNK	cardioexcitatory n
39	6	23.8	3	3	A32039	tyrosine-melanocyt
40	5	23.8	3	3	PQ0010	angiotensin-conver
41	5	23.8	3	3	S13894	histidinol dehydro
42	5	23.8	3	3	I50412	gene p20K protein
43	5	23.8	3	3	PT0578	T-cell receptor k
44	5	23.8	3	2	I78890	tyrosine protein k
44	5	23.8	4	3	T13892	cytochrome-c oxida
45	5	23.8	4	2	S18401	thyroglobulin - do

ALIGNMENTS

RESULT 1
PT0240
Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0240
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and jo
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0240
A;Molecule type: DNA
A;Residues: 1-4 <YAM>
A;Cross-references: UNIPARC:UPI000017C1E2
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match   47.6%; Score 10; DB 2; Length 4;
Best Local Similarity   100.0%; Pred. No. 2.8e+05;
Matches   2; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 GL 3
              |||
Db   3 GL 4

RESULT 2
A53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A53284
R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A;Title: Evolutionarily conserved organization and sequences of germline diversity and jo
A;Reference number: A53284; MUID:91342695; PMID:1678859
A;Accession: A53284
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4 <HAR>
A;Cross-references: UNIPARC:UPI00001E8F2; GB:S60737; NID:g233916; PIDN:AAB19517.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60739)
C;Keywords: T-cell receptor

Query Match   47.6%; Score 10; DB 2; Length 4;
Best Local Similarity   100.0%; Pred. No. 2.8e+05;
Matches   2; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2 GL 3
              |||
Db   1 GL 2

RESULT 3
PT0633
T-cell receptor beta chain V-D-J region (120-2C) - mouse (fragment)
C;Species: Mus musculus (house mouse)
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0633
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0633
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FEB>
A;Cross-references: UNIPARC:UPI000017C7DF
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match   38.1%; Score 8; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy   2 GL 3
             :|
Db   3 GI 4

RESULT 4
B23751
spinal cord peptide SCP-5 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001
C;Accession: B23751
R;Hsi, K.L.; Chen, R.L.; Zhang, Z.G.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K
Arch. Biochem. Biophys. 240, 178-183, 1985
A;Reference number: A23751; MUID:85250425; PMID:4015098
A;Accession: B23751
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-3 <HSI>
A;Cross-references: UNIPARC:UPI000017CE98

Query Match   33.3%; Score 8; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy   3 LM 4
             :|
Db   1 MM 2

RESULT 5
E44823
synaptosomal-associated protein SNAP-25 peptide 1 - rabbit (fragment)
N;Alternate names: superprotein peptide 1
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C;Accession: E44823
R;Loewy, A.; Liu, W.S.; Baltinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A;Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
A;Reference number: A44823; MUID:9204785; PMID:1941090
A;Accession: E44823
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-4 <LOE>
A;Cross-references: UNIPARC:UPI000017C5E3
A;Experimental source: visual tissue
A;Note: sequence extracted from NCBI backbone (NCBIP:64247)
C;Keywords: membrane trafficking

Query Match   33.3%; Score 7; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy   3 LM 4
             :|
Db   1 IM 2

RESULT 6
B53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: B53284
R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A;Title: Evolutionarily conserved organization and sequences of germline diversity and j
A;Reference number: A53284; MUID:91342695; PMID:1678859
A;Accession: B53284
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4 <HAR>
A;Cross-references: UNIPARC:UPI00001E8F3; GB:S60737; NID:g239916; PIDN:AAB19518.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)
C;Keywords: T-cell receptor

Query Match   33.3%; Score 7; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy   1 FG 2
             :|
Db   2 WG 3

RESULT 7
PT0636
T-cell receptor beta chain V-D-J region (100-2AT) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PT0636
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0636
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-3 <FEE>
A;Cross-references: UNIPARC:UPI000017CE9E
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match   28.6%; Score 6; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   2 G 2
             |
Db   3 G 3

RESULT 8
PT0571
T-cell receptor beta chain V-D-J region (141-1CM) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PT0571
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0571

OM protein - protein search, using sw model

Run on: November 26, 2005, 02:27:59 ; Search time 225 Seconds

GenCore version 5.1.6
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Title:
Perfect score: US-10-805-881-2
Sequence: 21
     1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 32

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

(without alignments)
12.543 Million cell updates/sec

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	12	57.1	4	1	OCP1_OCTMI	P58648; octopus min
2	9	42.9	4	1	ILME_SEPOF	P83568; sepia offic
3	6	28.6	2	1	GWA_SEPOF	P83570; sepia offic
4	6	28.6	3	1	GRWM_HUMAN	P01157; homo sapien
5	6	28.6	4	1	ACH1_ACHFU	P35904; achatina fu
6	6	28.6	4	1	DCML_PSECH	P19916; pseudomonas
7	6	28.6	4	1	EOS1_HUMAN	P02731; homo sapien
8	6	28.6	4	1	OCP3_OCTMI	P02731; homo sapien
9	6	28.6	4	1	FAR3_HIRME	P42562; hirudo medi
10	6	28.6	4	1	FAR4_HIRME	P42563; hirudo medi
11	6	28.6	4	1	FFKA_ANTEL	P58705; anthopleura
12	6	28.6	4	1	FLRF_HELTI	P58707; helisoma tr
13	6	28.6	4	1	FLRN_ANTEL	P58707; anthopleura
14	6	28.6	4	1	FMRF_HELTI	P69148; helisoma tr
15	6	28.6	4	1	FMRF_HIRME	P69147; hirudo medi
16	6	28.6	4	1	FMRF_MACNI	P69145; macrocallis
17	6	28.6	4	1	FMRF_NERVI	P69146; nereis vire
18	6	28.6	4	1	FYRI_ANTEL	P58706; anthopleura
19	6	28.6	4	1	EOSI_HUMAN	P58649; octopus min
20	6	28.6	4	1	TPAN1_PANIM	P84465; pandinus im
21	6	28.6	4	2	Q16047_HUMAN	Q16047; homo sapien
22	5	28.6	4	2	DCMS_PSECH	P19918; pseudomonas
23	5	23.8	4	1	Q96AT0_HUMAN	Q96at0; homo sapien
24	4	19.0	2	1	TPAN2_PANIM	P84464; pandinus im
25	4	19.0	2	1	Q08433_9MURI	Q08433; rattus sp.
26	2	9.5	3	1	LUXE_VIBFI	Q24272; vibrio fisc
27	1	4.8	3	1	YLM1_YEAST	P36515; saccharomyc
28	0	0.0	3	1	THYL_BOMOR	P62970; bombina ori
29	0	0.0	3	1	THYL_NOTVI	P62971; notophthalm
30	0	0.0	3	1	THYL_PIG	P62968; sus scrofa
31	0	0.0	3	1	THYL_SHEEP	P62969; ovis aries

---

32   0   0.0   4   1   TUFT_HUMAN   P01858 homo sapien

ALIGNMENTS

RESULT 1
OCP1_OCTMI
ID   OCP1_OCTMI   STANDARD;   PRT;   4 AA.
AC   P58648;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Cardioactive peptides Ocp-1/Ocp-2.
OS   Octopus minor (Octopus).
OC   Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC   Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX   NCBI_TaxID=99766;
RN   [1]
RP   PROTEIN SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC   TISSUE=Brain;
RX   MEDLINE=20336815; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;
RA   Iwakoshi E., Hisada M., Minakata H.;
RT   "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT   Octopus minor.";
RL   Peptides 21:623-630(2000).
CC   -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC   inotropic effects on the heart. Ocp-2 is a 1000 time less active
CC   than Ocp-1.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: Ocp-2 has L-Phe instead of D-Phe.
CC   -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.
CC   -!--
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -!--
KW   D-amino acid; Direct protein sequencing; Hormone.
FT   MOD_RES   2   2   D-phenylalanine (in form Ocp-1).
SQ   SEQUENCE   4 AA;   394 MW;   6AA879C810000000 CRC64;

Query Match   57.1%;   Score 12;   DB 1;   Length 4;
Best Local Similarity   100.0%;   Pred. No. 2.2e+06;
Matches   2;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 FG 2
       ||
Db   2 FG 3

RESULT 2
ILME_SEPOF
ID   ILME_SEPOF   STANDARD;   PRT;   4 AA.
AC   P83568;
DT   29-MAR-2004 (Rel. 43, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Pheromone peptide ILME.
OS   Sepia officinalis (Common cuttlefish).
OC   Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC   Decapodiformes; Sepioidea; Sepiidae; Sepia.
OX   NCBI_TaxID=6610;
RN   [1]
RP   PROTEIN SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
RP   SPECTROMETRY.
RC   TISSUE=Egg;
RX   MEDLINE=20403899; PubMed=10944467; DOI=10.1006/bbrc.2000.3286;
RA   Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;
RT   "ILME: a waterborne pheromonal peptide released by the eggs of Sepia
RT   officinalis.";
RL   Biochem. Biophys. Res. Commun. 275:217-222(2000).

RN [2]
RP PROTEIN SEQUENCE.
RC TISSUE=Egg;
RX MEDLINE=2219710B; PubMed=12207899; DOI=10.1016/S0006-291X(02)02036-3;
RA Zatylny C., Marvin L., Gagnon J., Henry J.;
RT "Fertilization in Sepia officinalis: the first mollusk sperm-
RT attracting peptide.";
RL Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
CC -!- FUNCTION: Has myotropic activity targeting the genital tract.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Follicle, fully grown oocyte and egg(EC2).
CC -!- MASS SPECTROMETRY: MW=505.4; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.
CC ---
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC ---
KW Direct protein sequencing; Pheromone.
SQ SEQUENCE   4 AA; 505 MW; 6B1697203000000 CRC64;

Qy   3 LM 4
                 | |
Db   2 LM 3

Query Match   42.9%; Score 9; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches   2; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 3
ID GWA_SEPOF   STANDARD;   PRT;   2 AA.
AC P83570;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neuropeptide GWa.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP PROTEIN SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Optic lobe;
RX MEDLINE=98100358; PubMed=9437704; DOI=10.1016/S0196-9781(97)00241-6;
RA Henry J., Favrel P., Boucaud-Camou E.;
RT "Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related
RT peptide inhibiting the motility of the mature oviduct in the
RT cuttlefish, Sepia officinalis.";
RL Peptides 18:1469-1474(1997).
CC -!- FUNCTION: Regulatory neuropeptide with myotropic activity
CC   targeting the distal oviduct. Inhibits the motility of the oviduct
CC   by decreasing tonus, frequency and amplitude of contractions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI; RANGE=1-2; NOTE=Ref.1.
CC ---
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC ---
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES   2   2   Tryptophan amide.
SQ SEQUENCE   2 AA; 261 MW; 7378100000000 CRC64;

Qy   2 G 2

Query Match   28.6%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches   1; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 4
ID GRWM_HUMAN   STANDARD;   PRT;   3 AA.
AC P01157;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Growth-modulating peptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=77162369; PubMed=858356;
RA Schlesinger D.H., Pickart L., Thaler M.M.;
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL Experientia 33:324-325(1977).
CC -!- MISCELLANEOUS: This serum tripeptide has been found to stimulate
CC   growth of some cell types and to inhibit other types in vitro.
CC ---
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC ---
DR GO; GO:0001558; P:regulation of cell growth; NAS.
KW Direct protein sequencing.
SQ SEQUENCE   3 AA; 340 MW; 6331B8100000000000 CRC64;

Qy   2 G 2
                 |
Db   1 G 1

Query Match   28.6%; Score 6; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches   1; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 5
ID ACH1_ACHFU   STANDARD;   PRT;   4 AA.
AC P35004;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Achatin-I.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP PROTEIN SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RC STRAIN=Ferussac; TISSUE=Ganglion;
RX MEDLINE=89273551; PubMed=2597281;
RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
RT fulica Ferussac containing a D-amino acid residue.";
RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
RN [2]
RP CHARACTERIZATION.
RC STRAIN=Ferussac; TISSUE=Heart atrium;
RX MEDLINE=91264856; PubMed=1675568;
RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;

OM protein - protein search, using sw model

```
                          GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.
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Run on: November 26, 2005, 02:31:00

Title: US-10-805-881-2
Perfect score: 21
Sequence: 1 PGIM 4
Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5
Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 13782

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                SUMMARIES

; Search time 45 Seconds
; (without alignments)
; 7.349 Million cell updates/sec

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	4	1	US-08-441-591-63	Sequence 63, Appl
2	21	100.0	4	1	US-08-303-362A-63	Sequence 63, Appl
3	21	100.0	4	2	US-09-265-690C-2	Sequence 2, Appli
4	21	100.0	4	2	US-09-665-362A-31	Sequence 31, Appli
5	21	100.0	4	2	US-10-230-133-3	Sequence 3, Appli
6	21	100.0	4	2	US-09-623-548A-623	Sequence 623, Appli
7	21	100.0	4	2	US-10-695-536-3	Sequence 3, App
8	21	100.0	4	2	US-09-657-276-623	Sequence 623, App
9	21	100.0	4	4	PCT-US95-05600-80	Sequence 80, Appl
10	16	100.0	4	4	US-08-747-137-124	Sequence 124, Appl
11	16	76.2	4	1	US-08-722-126A-20	Sequence 20, Appl
12	16	71.4	3	2	US-09-635-266-2	Sequence 2, Appli
13	15	71.4	3	2	US-10-230-133-2	Sequence 2, Appli
14	15	71.4	3	2	US-09-623-548A-624	Sequence 624, App
15	15	71.4	3	2	US-09-657-276-624	Sequence 624, App
16	15	71.4	3	2	US-10-695-536-2	Sequence 2, Appli
17	15	71.4	4	1	US-08-070-301-8	Sequence 8, Appli
18	15	71.4	4	1	US-08-433-401-4	Sequence 4, Appli
19	15	71.4	4	2	US-09-623-548A-971	Sequence 971, App
20	15	71.4	4	2	US-09-623-548A-998	Sequence 998, App
21	15	71.4	4	2	US-09-657-276-971	Sequence 971, App
22	15	71.4	4	2	US-09-657-276-998	Sequence 998, App
23	14	71.4	4	2	US-08-793-701-25	Sequence 25, Appl
24	14	66.7	4	2	US-09-579-264-25	Sequence 25, Appl
25	14	66.7	4	2	US-09-623-548A-890	Sequence 890, App
26	14	66.7	4	2	US-09-657-276-890	Sequence 890, App
27	13	61.9	4	1	US-08-429-964-37	Sequence 37, Appl
28	13	61.9	4	2	US-08-812-586-60	Sequence 60, Appl
29	13	61.9	4	2	US-08-669-656A-11	Sequence 11, Appl
30	13	61.9	4	2	US-09-535-832A-56	Sequence 56, Appl
31	13	61.9	4	2	US-09-665-362A-31	Sequence 31, Appl
32	13	61.9	4	2	US-09-665-637-31	Sequence 31, Appl
33	13	61.9	4	2	US-10-087-402-10	Sequence 10, Appl
34	13	61.9	4	2	US-10-083-894-31	Sequence 31, Appl
35	13	61.9	4	4	PCT-US93-08062-37	Sequence 37, Appl
36	12	57.1	3	1	US-08-343-943-4	Sequence 4, Appl
37	12	57.1	3	2	US-09-060-455-2	Sequence 2, Appl
38	12	57.1	3	2	US-09-150-621-3	Sequence 3, Appli
39	12	57.1	3	2	US-10-121-857-6	Sequence 6, Appli
40	12	57.1	3	2	US-09-623-548A-1527	Sequence 1527, Appli
41	12	57.1	3	2	US-09-657-276-1527	Sequence 1527, Ap
42	12	57.1	3	2	US-07-657-769B-58	Sequence 58, Appli
43	12	57.1	4	1	US-07-822-924-3	Sequence 3, Appli
44	12	57.1	4	1	US-07-822-924-5	Sequence 5, Appli
45	12	57.1	4	1	US-07-822-924-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-441-591-63
Sequence 63, Application US/08441591
; Patent No. 5637682
; GENERAL INFORMATION:
; APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.
; TITLE OF INVENTION: HIGH-AFFINITY
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
; TITLE OF INVENTION: TO THE TACHYKININ
; TITLE OF INVENTION: SUBSTANCE P
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,591
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/303,362
; FILING DATE: 9-SEPTEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 8-SEPTEMBER 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX21/C
; TELECOMMUNICATION INFORMATION:

```
;     TELEPHONE:  (303) 793-3333
;     TELEFAX:  (303) 793-3433
; INFORMATION FOR SEQ ID NO: 63:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  4
;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
US-08-441-591-63

Qy          100.0%; Score 21; DB 1; Length 4;
Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 FGLM 4
        ||||
Db    1 FGLM 4
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RESULT 2
US-08-303-362A-63
Sequence 63, Application US/0830336 2A
Patent No. 5648214
; GENERAL INFORMATION:
;   APPLICANT: NIEUWLANDT, D.; GOLD, L. AND WECKER, M.
;   TITLE OF INVENTION: HIGH-AFFINITY
;   TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
;   TITLE OF INVENTION: TO THE TACHYKININ
;   TITLE OF INVENTION: SUBSTANCE P
;   NUMBER OF SEQUENCES: 66
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Swanson & Bratschun, L.L.C.
;   STREET: 8400 E. Prentice Avenue, Suite 200
;   CITY: Englewood
;   STATE: Colorado
;   COUNTRY: USA
;   ZIP: 80111
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
;   COMPUTER: IBM compatible
;   OPERATING SYSTEM: MS-DOS
;   SOFTWARE: WordPerfect 5.1
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/303,362A
;   FILING DATE: 9-SEPTEMBER-1994
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/714,131
;   FILING DATE: 10-JUNE-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/931,473
;   FILING DATE: 17-AUGUST-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/117,991
;   FILING DATE: 8-SEPTEMBER 1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/536,428
;   FILING DATE: 11-JUNE-1990
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/964,624
;   FILING DATE: 21-OCTOBER-1992
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Barry J. Swanson
;   REGISTRATION NUMBER: 33,215
;   REFERENCE/DOCKET NUMBER: NEX21
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (303) 793-3333
;   TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 63:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 4
;   TYPE: amino acid
;   STRANDEDNESS: single

; TOPOLOGY: linear
US-08-303-362A-63

Qy   100.0%; Score 21; DB 1; Length 4;
Best Local Similarity   100.0%; Pred. No. 4.6e+05;
Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FGLM 4
        ||||
Db   1 FGLM 4

RESULT 3
US-09-265-690C-2
Sequence 2, Application US/09265690C
Patent No. 6372440
; GENERAL INFORMATION:
;   APPLICANT: Wells, Ibert
;   TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
;   TITLE OF INVENTION: for Disease Diagnosis
;   FILE REFERENCE: 1427001
;   CURRENT APPLICATION NUMBER: US/09/265,690C
;   CURRENT FILING DATE: 1999-03-10
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (4)..(4)
;   OTHER INFORMATION: AMIDATION
US-09-265-690C-2

Qy   100.0%; Score 21; DB 2; Length 4;
Best Local Similarity   100.0%; Pred. No. 4.6e+05;
Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FGLM 4
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Db   1 FGLM 4

RESULT 4
US-09-635-266-3
Sequence 3, Application US/09635266
Patent No. 6455734
; GENERAL INFORMATION:
;   APPLICANT: Wells, Ibert
;   TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
;   TITLE OF INVENTION: methods for treatment of abnormal physiological states
;   FILE REFERENCE: N1427-002
;   CURRENT APPLICATION NUMBER: US/09/635,266
;   CURRENT FILING DATE: 2000-08-09
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (4)..(4)
;   OTHER INFORMATION: AMIDATION
US-09-635-266-3

Qy   100.0%; Score 21; DB 2; Length 4;
Best Local Similarity   100.0%; Pred. No. 4.6e+05;
Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FGLM 4
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OM protein - protein search, using sw model

Copyright (c) 1993 - 2005 Compugen Ltd.

GenCore version 5.1.6

Run on: November 26, 2005, 02:38:10 ; Search time 159 Seconds
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Title: US-10-805-881-2
Perfect score: 21
Sequence: 1 FGLM 4
Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5
Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 13481

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	21	100.0	4	3	US-09-265-690C-2	Sequence 2, Appli
2	21	100.0	4	4	US-10-230-133-3	Sequence 3, Appli
3	21	100.0	4	4	US-10-053-669-2	Sequence 2, Appli
4	21	100.0	4	4	US-10-695-536-3	Sequence 3, Appl
5	21	100.0	4	4	US-10-805-881-2	Sequence 2, Appli
6	21	100.0	4	5	US-10-497-628-2	Sequence 2, Appli
7	21	100.0	4	4	US-10-805-690-3	Sequence 2, Appli
8	21	100.0	4	6	US-11-018-690-3	Sequence 3, App
9	21	100.0	4	6	US-11-066-697-623	Sequence 623, App
10	16	76.2	4	3	US-09-879-442A-9	Sequence 9, Appli
11	16	76.2	4	5	US-10-821-240A-270	Sequence 270, App
12	15	71.4	3	4	US-10-230-133-2	Sequence 2, Appli
13	15	71.4	3	4	US-10-695-536-2	Sequence 2, Appli
14	15	71.4	3	6	US-11-018-690-2	Sequence 2, Appli
15	15	71.4	4	6	US-11-066-697-624	Sequence 624, App
16	15	71.4	4	6	US-11-066-697-971	Sequence 971, App
17	14	66.7	4	6	US-11-066-697-998	Sequence 998, App
18	14	66.7	5	5	US-09-879-442A-8	Sequence 8, Appli
19	14	66.7	5	6	US-10-137-867-328	Sequence 328, App
20	14	66.7	5	6	US-10-433-709-17	Sequence 17, Appl
21	13	61.9	6	6	US-11-066-697-890	Sequence 890, App
22	13	61.9	3	6	US-09-943-123-24	Sequence 24, Appl
23	13	61.9	3	5	US-09-879-442A-99	Sequence 99, Appl
24	13	61.9	4	4	US-10-087-905-30	Sequence 30, Appl
25	13	61.9	4	4	US-10-087-402-10	Sequence 10, Appl
26	13	61.9	4	4	US-10-083-894-31	Sequence 31, Appl
27	13	61.9	4	4		
28	13	61.9	4	4	US-10-196-394-98	Sequence 98, Appl
29	13	61.9	4	4	US-10-202-824-11	Sequence 11, Appl
30	13	61.9	4	4	US-10-359-363A-104	Sequence 104, App
31	13	61.9	4	4	US-10-491-418-21	Sequence 21, Appl
32	13	61.9	4	5	US-10-712-359A-24	Sequence 24, Appl
33	13	61.9	4	5	US-10-476-861A-11	Sequence 11, Appl
34	13	61.9	4	5	US-10-476-861A-118	Sequence 118, App
35	13	61.9	4	6	US-11-136-464-11	Sequence 11, Appl
36	13	57.1	4	6	US-10-121-857-6	Sequence 6, Appli
37	13	57.1	4	4	US-10-255-679-3	Sequence 3, Appli
38	12	57.1	4	6	US-10-208-018-6	Sequence 6, Appli
39	12	57.1	4	6	US-10-104-307-3	Sequence 3, Appli
40	12	57.1	3	6	US-11-066-697-1527	Sequence 1527, Ap
41	12	57.1	3	6	US-08-484-409-14	Sequence 14, Appl
42	12	57.1	4	6	US-08-484-409-25	Sequence 25, Appl
43	12	57.1	4	3	US-09-804-733A-24	Sequence 24, Appl
44	12	57.1	4	3	US-09-803-126-20	Sequence 20, Appl
45	12	57.1	4	3	US-09-726-470A-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
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; Sequence 2, Application US/09265690C
; Publication No. US20010051345A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mag
; TITLE OF INVENTION: for Disease Diagnosis
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265,690C
; CURRENT FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: AMIDATION
US-09-265-690C-2

Query Match   100.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
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Qy   1 FGLM 4
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Db   1 FGLM 4

RESULT 2
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; Sequence 3, Application US/10230133
; Publication No. US20030040625A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
; TITLE OF INVENTION: methods for treatment of abnormal physiological states
; FILE REFERENCE: 2892-106
; CURRENT APPLICATION NUMBER: US/10/230,133
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 09/635,266
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT

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;       ORGANISM: Homo sapiens
;       FEATURE:
;          NAME/KEY: MOD_RES
;          LOCATION: (4)..(4)
;          OTHER INFORMATION: AMIDATION
US-10-230-133-3

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Db        1   FGLM   4
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RESULT 3
US-10-053-669-2
Sequence 2, Application US/10053669
Publication No. US20030077658A1
GENERAL INFORMATION:
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;       APPLICANT: Wells, Ibert
;       TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
;       FILE REFERENCE: N1427-005
;       CURRENT APPLICATION NUMBER: US/10/053,669
;       CURRENT FILING DATE: 2002-01-24
;       PRIOR APPLICATION NUMBER: 09/265,690
;       PRIOR FILING DATE: 1999-03-10
;       NUMBER OF SEQ ID NOS: 4
;       SOFTWARE: Patentin version 3.0
;       SEQ ID NO 2
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;       TYPE: PRT
;       ORGANISM: Homo sapiens
;       FEATURE:
;          NAME/KEY: MOD_RES
;          LOCATION: (4)..(4)
;          OTHER INFORMATION: AMIDATION
US-10-053-669-2
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Query Match   100.0%;   Score 21;   DB 4;   Length 4;
Best Local Similarity 100.0%;   Pred. No. 1.7e+06;
Matches   4;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy        1   FGLM   4
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RESULT 4
US-10-695-536-3
Sequence 3, Application US/10695536
Publication No. US20040110692A1
GENERAL INFORMATION:
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;       APPLICANT: Wells, Ibert Clifton
;       TITLE OF INVENTION: Antagonists of the Magnesium Binding Defect as Therapeutic Agents
;       TITLE OF INVENTION: and Methods for Treatment of Abnormal Physiological States
;       FILE REFERENCE: 800812-0008
;       CURRENT APPLICATION NUMBER: US/10/695,536
;       CURRENT FILING DATE: 2003-10-28
;       PRIOR APPLICATION NUMBER: US 10/230,133
;       PRIOR FILING DATE: 2002-08-29
;       PRIOR APPLICATION NUMBER: US 09/635,266
;       PRIOR FILING DATE: 2000-08-09
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US-10-695-536-3

Qy        1   FGLM   4
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RESULT 5
US-10-805-881-2
Sequence 2, Application US/10805881
Publication No. US20040171093A1
GENERAL INFORMATION:
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;       APPLICANT: Wells, Ibert C.
;       TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound
;       TITLE OF INVENTION: Magnesium for Disease Diagnosis
;       FILE REFERENCE: 800812-0005
;       CURRENT APPLICATION NUMBER: US/10/805,881
;       CURRENT FILING DATE: 2004-03-22
;       PRIOR APPLICATION NUMBER: US 10/053,669
;       PRIOR FILING DATE: 2002-01-24
;       PRIOR APPLICATION NUMBER: US 10/695,536
;       PRIOR FILING DATE: 2003-10-28
;       NUMBER OF SEQ ID NOS: 4
;       SOFTWARE: Patentin version 3.2
;       SEQ ID NO 2
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;       FEATURE:
;          NAME/KEY: MOD_RES
;          LOCATION: (4)..(4)
;          OTHER INFORMATION: AMIDATION
US-10-805-881-2
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Query Match   100.0%;   Score 21;   DB 4;   Length 4;
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Db        1   FGLM   4
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RESULT 6
US-10-497-628-2
Sequence 2, Application US/10497628
Publication No. US20050009752A1
GENERAL INFORMATION:
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;       APPLICANT: Teruo Nishida
;       APPLICANT: Makoto Inui
;       APPLICANT: Masatsugu Nakamura
;       TITLE OF INVENTION: NOVEL PEPTIDE AND PHARMACEUTICAL USE OF THE SAME
;       FILE REFERENCE: 0435S/HG
;       CURRENT APPLICATION NUMBER: US/10/497,628
;       CURRENT FILING DATE: 2004-06-03
;       PRIOR APPLICATION NUMBER: JP 2001-368103
;       PRIOR FILING DATE: 2001-12-01
;       NUMBER OF SEQ ID NOS: 17
;       SOFTWARE: Patentin Ver. 2.1
;       SEQ ID NO 2
;       LENGTH: 4
;       TYPE: PRT
;       ORGANISM: Human
US-10-497-628-2
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Query Match   100.0%;   Score 21;   DB 5;   Length 4;
Best Local Similarity 100.0%;   Pred. No. 1.7e+06;

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: November 26, 2005, 02:38:51 ; Search time 8 Seconds
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1.515 Million cell updates/sec

Title: US-10-805-881-2
Perfect score: 21
Sequence: 1 FGLM 4
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 94

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

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2	10	47.6	4	7	US-11-046-644-27	Sequence 27, Appl
3	10	47.6	4	7	US-11-052-168A-38	Sequence 38, Appl
4	8	38.1	4	7	US-11-064-785-1	Sequence 1, Appli
5	7	33.3	4	7	US-10-977-367-21	Sequence 21, Appl
6	7	33.3	4	1	US-10-977-367-36	Sequence 36, Appl
7	7	33.3	4	1	US-10-997-066-16	Sequence 16, Appl
8	7	33.3	4	1	US-11-035-682-12	Sequence 12, Appl
9	6	28.6	3	7	US-11-052-168A-4	Sequence 4, Appli
10	6	28.6	3	7	US-11-052-168A-39	Sequence 39, Appl
11	6	28.6	4	7	US-10-503-575-48	Sequence 48, Appl
12	6	28.6	4	7	US-10-503-575-49	Sequence 49, Appl
13	6	28.6	4	1	US-10-503-575-59	Sequence 59, Appl
14	6	28.6	4	1	US-10-503-575-62	Sequence 62, Appl
15	6	28.6	4	1	US-10-977-367-1	Sequence 1, Appli
16	6	28.6	4	1	US-10-979-821-77	Sequence 77, Appl
17	6	28.6	4	1	US-10-997-066-16	Sequence 16, Appl
18	6	28.6	4	1	US-10-939-890-18	Sequence 18, Appl
19	6	28.6	4	1	US-10-939-890-262	Sequence 262, App
20	6	28.6	4	1	US-10-939-890-791	Sequence 791, App
21	6	28.6	4	1	US-10-939-890-792	Sequence 792, App
22	6	28.6	4	1	US-10-939-890-871	Sequence 871, App
23	6	28.6	4	1	US-10-966-648-28	Sequence 28, Appl
24	6	28.6	4	1	US-10-484-271A-7	Sequence 7, Appli
25	6	28.6	4	1	US-10-516-768-38	Sequence 38, Appl
26	6	28.6	4	1	US-10-997-759-57	Sequence 57, Appl
27	6	28.6	4	7	US-11-016-503-26	Sequence 26, Appl
28	6	28.6	4	7	US-11-176-868-27	Sequence 27, Appl
29	6	28.6	4	7	US-11-176-868-36	Sequence 36, Appl
30	6	28.6	4	7	US-11-176-868-39	Sequence 39, Appl
31	6	28.6	4	7	US-11-010-954-27	Sequence 27, Appl
32	6	28.6	4	7	US-11-022-289-15	Sequence 15, Appl
33	6	28.6	4	7	US-11-033-365-53	Sequence 53, Appl
34	6	28.6	4	7	US-11-052-168A-2	Sequence 2, Appli
35	6	28.6	4	7	US-11-053-100-1	Sequence 1, Appli
36	6	28.6	4	7	US-11-053-100-2	Sequence 2, Appli
37	5	23.8	4	7	US-11-053-750-27	Sequence 27, Appl
38	6	28.6	4	7	US-10-845-413-154	Sequence 154, App
39	5	23.8	5	7	US-11-053-575-61	Sequence 61, Appl
40	4	19.0	4	1	US-11-113-224-57	Sequence 57, Appl
41	4	19.0	4	1	US-11-113-224-59	Sequence 59, Appl
42	4	19.0	4	1	US-10-444-662-3	Sequence 3, Appli
43	4	19.0	4	1	US-10-667-295-262	Sequence 262, App
44	4	19.0	4	1	US-10-667-295-263	Sequence 263, App
45	4	19.0	4	7	US-11-011-666-14	Sequence 14, Appl
					US-11-016-503-35	Sequence 35, Appl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-11-046-456-27

; Sequence 27, Application US/11046456
; Publication No. US20050250044A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, Bryan
; APPLICANT: Funk, Walter
; APPLICANT: Kakitani, Makoto
; APPLICANT: Oshima, Takeshi
; APPLICANT: Park, Eun Ju
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yagi, Mikio
; APPLICANT: Tomizuka, Kazuma
; TITLE OF INVENTION: Gastrointestinal Proliferative Factor and uses thereof
; FILE REFERENCE: 18824-003001
; CURRENT APPLICATION NUMBER: US/11/046,456
; CURRENT FILING DATE: 2005-01-27
; PRIOR APPLICATION NUMBER: US 60/539,605
; PRIOR FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: US 60/619,241
; PRIOR FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US 10/488,423
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: PCT/US02/27746
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 27
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-046-456-27

Query Match 47.6%; Score 10; DB 7; Length 4;
Best Local Similarity 66.7%;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GLM 4
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Db 2 GTM 4

RESULT 2
US-11-046-644-27

; Sequence 27, Application US/11046644
; Publication No. US20050250036A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, Bryan

US-11-046-644-27
; ORGANISM: Homo sapiens
; TYPE: PRT
; LENGTH: 4
; SOFTWARE: Patentin version 3.3
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 27
; PRIOR FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US 60/619,241
; PRIOR FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: US 60/539,605
; CURRENT FILING DATE: 2005-01-27
; CURRENT APPLICATION NUMBER: US/11/046,644
; FILE REFERENCE: 11926-194001
; TITLE OF INVENTION: Gastrointestinal Proliferative Factor and uses thereof
; APPLICANT: Yagi, Mikio
; APPLICANT: Tomizuka, Kazuma
; APPLICANT: Tang, Y. Tom
; APPLICANT: Park, Emily
; APPLICANT: Oshima, Takeshi
; APPLICANT: Kakitani, Makoto
; APPLICANT: Funk, Walter

Query Match   47.6%;   Score 10; DB 7; Length 4;
Best Local Similarity   66.7%;   Pred. No. 1.5e+04;
Matches   2; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   2 GLM 4
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Db   2 GTM 4

RESULT 3
US-11-052-168A-38
Sequence 38, Application US/11052168A
Publication No. US20050253301A1
; GENERAL INFORMATION:
; APPLICANT: Craik, David James
; APPLICANT: Daly, Norelle Lee
; APPLICANT: Nielsen, Katherine Justine
; APPLICANT: Armishaw, Christopher
; APPLICANT: Clark, Richard James
; APPLICANT: Alewood, Paul Francis
; TITLE OF INVENTION: CYCLISED CONOTOXIN PEPTIDES
; FILE REFERENCE: DAVI-0008
; CURRENT APPLICATION NUMBER: US/11/052,168A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 09/787,082
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: PCT/AU99/00769
; PRIOR FILING DATE: 1999-09-14
; PRIOR APPLICATION NUMBER: AU PP 5895
; PRIOR FILING DATE: 1998-09-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 38
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct

US-11-052-168A-38

Qy   2 GL 3
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Db   1 GL 2

RESULT 4

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Matches   2; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

US-11-064-785-1
Sequence 1, Application US/11064785
Publication No. US20050256030A1
; GENERAL INFORMATION:
; APPLICANT: FENG, BAINIAN
; TITLE OF INVENTION: HETEROCYCLIC SELF-IMMOLATIVE LINKERS AND
; TITLE OF INVENTION: CONJUGATES
; FILE REFERENCE: 39766-0143A
; CURRENT APPLICATION NUMBER: US/11/064,785
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US 60/547,152
; PRIOR FILING DATE: 2004-02-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-064-785-1

Query Match   38.1%;   Score 8; DB 7; Length 4;
Best Local Similarity   33.3%;   Pred. No. 1.5e+04;
Matches   1; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   2 GLM 4
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Db   1 GFL 3

RESULT 5
US-10-977-367-21
Sequence 21, Application US/10977367
Publication No. US20050245445A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Hanahan, Douglas
; TITLE OF INVENTION: Molecules That Selectively Home To
; TITLE OF INVENTION: Vasculature of Premalignant or Malignant Lesions of the
; TITLE OF INVENTION: Pancreas and Other Organs
; FILE REFERENCE: 66821-310
; CURRENT APPLICATION NUMBER: US/10/977,367
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: 60/516,118
; PRIOR FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-977-367-21

Query Match   33.3%;   Score 7; DB 1; Length 4;
Best Local Similarity   50.0%;   Pred. No. 1.5e+04;
Matches   1; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   2 GL 3
              | :
Db   3 GV 4

RESULT 6
US-10-977-367-36
Sequence 36, Application US/10977367
Publication No. US20050245445A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Hanahan, Douglas
; TITLE OF INVENTION: Molecules That Selectively Home To

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: November 26, 2005, 03:02:43 ; Search time 75.3571 Seconds
(without alignments)
29.153 Million cell updates/sec

Title: US-10-805-881-4
Perfect score: 22
Sequence: 1 FXGLM 5
Scoring table: BLOSUM62
Searched: Gapop 10.0 , Gapext 0.5
2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 990051

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length	DB	ID	Description
1	21	95.5	9	9	ADV56611	Adv56611 G protein
2	21	95.5	9	9	ADV57296	Adv57296 G protein
3	21	95.5	12	2	AAW64648	Aaw64648 Synthetic
4	21	95.5	13	9	ADV57358	Adv57358 G protein
5	21	95.5	13	9	ADV56673	Adv56673 G protein
6	21	95.5	14	4	AAM97765	Aam97765 Human pep
7	21	95.5	15	8	ADL14251	Adl14251 Immunogen
8	21	95.5	15	8	ADL14262	Adl14262 Immunogen
9	21	95.5	15	8	ADL14261	Adl14261 Immunogen
10	21	95.5	15	8	ADL14263	Adl14263 Immunogen
11	21	95.5	19	8	ADV57350	Adv57350 G protein
12	21	95.5	19	9	ADV56665	Adv56665 G protein
13	21	95.5	20	2	AAW64649	Aaw64649 Synthetic
14	21	95.5	21	8	ADL14248	Adl14248 Immunogen
15	21	95.5	29	4	AAM14803	Aam14803 Peptide #
16	21	95.5	29	4	ABB33770	Abb33770 Peptide #
17	21	95.5	29	4	AAM27230	Aam27230 Peptide #
18	21	95.5	29	4	ABB28587	Abb28587 Peptide #
19	21	95.5	29	4	ABB19214	Abb19214 Protein #
20	21	95.5	29	4	AAM66943	Aam66943 Human bon
21	21	95.5	29	4	AAM54537	Aam54537 Human bra
22	21	95.5	29	4	ABG48607	Abg48607 Human liv
23	21	95.5	29	4	AAM02528	Aam02528 Peptide #
24	21	95.5	29	5	ABG36600	Abg36600 Human pep
25	20	90.9	5	2	AAR33009	Aar33009 Alpha-sub
26	20	90.9	5	2	AAR33008	Aar33008 Alpha-sub
27	20	90.9	5	2	AAR33007	Aar33007 Alpha-sub
28	20	90.9	5	2	AAR33010	Aar33010 Alpha-sub
29	20	90.9	5	2	AAW80134	Aaw80134 COOH-term
30	20	90.9	5	2	AAR54549	Aar54549 Cholecyst
31	20	90.9	5	2	AAR54551	Aar54551 Cholecyst
32	20	90.9	5	2	AAR54550	Aar54550 Cholecyst
33	20	90.9	5	2	AAR54548	Aar54548 Cholecyst
34	20	90.9	5	2	AAW41687	Aaw41687 Tetrapept
35	20	90.9	5	2	AAW99643	Aaw99643 Substance
36	20	90.9	5	2	AAY50325	Aay50325 Neutrophi
37	20	90.9	5	2	AAW92660	Aaw92660 Human tac
38	20	90.9	5	2	AAB23028	Aab23028 Mammalian
39	20	90.9	5	3	AAB23025	Aab23025 Human/rat
40	20	90.9	5	2	AAY67576	Aay67576 P antagon
41	20	90.9	5	2	AAB66674	Aab66674 C-termina
42	20	90.9	5	2	AAB82430	Aab82430 Fluorinat
43	20	90.9	5	2	AAB82431	Aab82431 Fluorinat
44	20	90.9	5	4	AAB91428	Aab91428 Tachykini
45	20	90.9	5	4	AAB70556	Aab70556 Octopus t

ALIGNMENTS

RESULT 1
ADV56611
ID   ADV56611 standard; peptide; 9 AA.
AC   ADV56611;
XX
DT   10-MAR-2005 (first entry)
XX
DE   G protein coupled receptor peptide SEQ ID NO 4113.
XX
KW   diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KW   food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX
OS   Unidentified.
XX
PN   WO2004111636-A2.
XX
PD   23-DEC-2004.
XX
PF   17-JUN-2004; 2004WO-EP051158.
XX
PR   17-JUN-2003; 2003EP-00101775.
PR   17-JUN-2003; 2003US-0479061P.
XX
PA   (VIBV-) VIB VZW.
PA   (UYGE-) UNIV GENT.
XX
PI   Kas K, Vandekerckhove J, Krols L;
XX
DR   WPI; 2005-057893/06.
XX
PT   Identifying a peptide combo which corresponds with a family of proteins,
PT   useful for diagnosing a variety of diseases, drug development or in
PT   agriculture, comprises generating peptides by applying a digest on the
PT   family of protein.
XX
PS   Example; SEQ ID NO 4113; 265pp; English.
XX
CC   The invention relates to a method of identifying a peptide combo which
CC   corresponds with a family of proteins where each of the members of the
CC   peptide combo is derived from a unique protein from the family. The
CC   peptide combo is useful for quantifying specific known splice variants of
CC   one or more particular proteins in a sample, for diagnosing complex
CC   genetic diseases such as cancer, obesity, diabetes, asthma and
CC   inflammation, neuropsychiatric disorders such as depression, for
CC   quantifying one to several hundreds of protein disease markers,
CC   simultaneously leading to a more accurate diagnostic sub-classification,

Left column

```
CC   for determining the extent of protein modification in a particular sample
CC   of proteins, for tissue-typing analysis, for prenatal testing to detect
CC   the presence of a congenital disease or for quantitating protein levels
CC   diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC   or neurological diseases, as biomarkers preclinical drug development,
CC   development of improved animal models, biomarkers related with
CC   toxicology, clinical drug development, guidance marketed drugs,
CC   prognostic or diagnostic disease markers, drug target validation and
CC   selection, monitoring protein splicing, drug lead profiling, pathway
CC   analysis, answering basic disease biology questions, and in the fields of
CC   food and feed, cosmetics, agriculture and animal breeding. The present
CC   sequence represents a peptide from a G-protein coupled receptor peptide
CC   combo.
XX
Qy
Db
SQ   Sequence 9 AA;

       Qy   1 FXGLM 5
                |||
       Db   1 FTGLM 5

Query Match      95.5%;   Score 21;  DB 9;  Length 9;
Best Local Similarity   80.0%;   Pred. No. 2e+06;
Matches    4;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

RESULT 2
ID   ADV57296 standard; peptide; 9 AA.
XX
AC   ADV57296;
XX
DT   10-MAR-2005  (first entry)
XX
DE   G protein coupled receptor peptide SEQ ID NO 4800.
XX
KW   diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KW   food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX
OS   Unidentified.
XX
PN   WO200411636-A2.
XX
PD   23-DEC-2004.
XX
DT   17-JUN-2004; 2004WO-EP051158.
PF   17-JUN-2003; 2003EP-00101775.
PR   17-JUN-2003; 2003US-0479061P.
XX
PA   (VIBV-) VIB VZW.
PA   (UYGE-) UNIV GENT.
XX
PI   Kas K, Vandekerckhove J, Krols L;
XX
DR   WPI; 2005-057893/06.
XX
PT   Identifying a peptide combo which corresponds with a family of proteins,
PT   useful for diagnosing a variety of diseases, drug development or in
PT   agriculture, comprises generating peptides by applying a digest on the
PT   family of protein.
PS   Example; SEQ ID NO 4800; 265pp; English.
XX
PT   The invention relates to a method of identifying a peptide combo which
CC   corresponds with a family of proteins where each of the members of the
CC   peptide combo is derived from a unique protein from the family. The
CC   peptide combo is useful for quantifying specific known splice variants of
CC   one or more particular proteins in a sample, for diagnosing complex
CC   genetic diseases such as cancer, obesity, diabetes, asthma and
CC   inflammation, neuropsychiatric disorders such as depression, for
CC   quantifying one to several hundreds of protein disease markers
CC   simultaneously leading to a more accurate diagnostic sub-classification,
CC   for determining the extent of protein modification in a particular sample
```

Right column

```
CC   of proteins, for tissue-typing analysis, for prenatal testing to detect
CC   the presence of a congenital disease or for quantitating protein levels
CC   diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC   or neurological diseases, as biomarkers preclinical drug development,
CC   development of improved animal models, biomarkers related with
CC   toxicology, clinical drug development, guidance marketed drugs,
CC   prognostic or diagnostic disease markers, drug target validation and
CC   selection, monitoring protein splicing, drug lead profiling, pathway
CC   analysis, answering basic disease biology questions, and in the fields of
CC   food and feed, cosmetics, agriculture and animal breeding. The present
CC   sequence represents a peptide from a G-protein coupled receptor peptide
CC   combo.
XX
Qy
Db
SQ   Sequence 9 AA;

       Qy   1 FXGLM 5
                |||
       Db   1 FTGLM 5

Query Match      95.5%;   Score 21;  DB 9;  Length 9;
Best Local Similarity   80.0%;   Pred. No. 2e+06;
Matches    4;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

RESULT 3
ID   AAW64648 standard; peptide; 12 AA.
XX
AC   AAW64648;
XX
DT   23-OCT-1998  (first entry)
XX
DE   Synthetic SEB-related peptide (position 13-24).
XX
KW   Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KW   toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW   therapeutic; vaccine; food poisoning.
XX
OS   Synthetic.
OS   Staphylococcus aureus.
XX
PN   WO9829444-A1.
XX
PD   09-JUL-1998.
XX
PF   30-DEC-1997; 97WO-IL000438.
PR   30-DEC-1996; 96IL-00119938.
XX
PA   (YISS ) YISSUM RES & DEV CO.
XX
PI   Kaempfer R, Arad G;
XX
DR   WPI; 1998-388042/33.
XX
PT   New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT   antagonising toxin-mediated activation of T cells and prevention or
PT   treatment of toxic shock caused by exotoxin(s).
PS   Example 2; Page 38; 68pp; English.
XX
PT   AAW64636-W64657 are peptides homologous to the amino acid sequence of a
CC   fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC   capable of eliciting protective immunity against toxic shock induced by
CC   PET or by a mixture of PETs. Such peptides are also capable of
CC   antagonising toxin-mediated activation of T-cells, inhibiting expression
CC   of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or TNF-
CC   beta genes. The peptides may be used to prepare therapeutics or vaccines
CC   for the treatment of prophylaxis of toxin-mediated activation of T cells
CC   and eliciting protective immunity against toxic shock induced by PETs.
CC   They can also be used for the treatment of harmful effects (especially
CC   food poisoning) and toxic shock caused by PET. Antiserum to the peptides
CC   can also be used for alleviating toxic shock induced by PET
```

OM protein - protein search, using sw model

```
                 GenCore version 5.1.6
           Copyright (c) 1993 - 2005  Compugen Ltd.
```

Run on: November 26, 2005, 03:18:04 ; Search time 20 Seconds
                                             (without alignments)
                                             24.054 Million cell updates/sec

Title: US-10-805-881-4
Perfect score: 22
Sequence: 1 FXGLM 5
Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 6683

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
                1: pir1:*
                2: pir2:*
                3: pir3:*
                4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	20	90.9	10	1	SPPGNK	neuromedin K - pig
2	20	90.9	10	2	JN0024	neurokinin A - chi
3	20	90.9	10	2	B49581	sialokinin II - ye
4	20	90.9	10	2	S23307	neurokinin A - rai
5	20	90.9	10	2	S23186	neurokinin A - Atl
6	20	90.9	10	2	S07202	phyllomedulin - tw
7	20	90.9	10	2	C61033	ranatachykinin C -
8	20	90.9	10	2	B61033	ranatachykinin B -
9	20	90.9	10	2	S27178	neurokinin A-relat
10	20	90.9	10	2	A49581	sialokinin I - yel
11	20	90.9	10	2	A24867	scyliorhinin I - s
12	20	90.9	10	2	A60654	substance P - guin
13	20	90.9	11	1	EOCC	eledoisin - musky
14	20	90.9	11	1	EOCCC	eledoisin - curled
15	20	90.9	11	1	SPHO	substance P - hors
16	20	90.9	11	1	JN0023	substance P - chic
17	20	90.9	11	2	S33300	probable substance
18	20	90.9	11	2	S07203	uperolein - frog (
19	20	90.9	11	2	C60409	kassinin-like pept
20	20	90.9	11	2	B60409	kassinin-like pept
21	20	90.9	11	2	B60409	substance P-like p
22	20	90.9	11	2	F60409	substance P-like p
23	20	90.9	11	2	S23308	kassinin-like pept
24	20	90.9	11	2	D60409	substance P - rain
25	20	90.9	11	2	S23306	substance P - Atla
26	20	90.9	11	2	S07201	physalaemin - frog
27	20	90.9	11	2	A61033	ranatachykinin A -
28	20	90.9	12	2	S10059	tachykinin - Afric
29	20	90.9	12	2	S07206	kassinin - Senegal
30	20	90.9	16	2	A60839	neurokinin A homol
31	20	90.9	18	2	B24867	scyliorhinin II -
32	20	90.9	21	2	JH0361	carassin - goldfis
33	18	81.8	12	2	S07436	tachykinin - Afric
34	18	81.8	28	1	LFEBLT	tachykinin -
35	18	81.8	28	2	AG0516	leu operon leader
36	18	81.8	30	2	F95118	leu operon leader
37	17	77.3	20	2	H49034	nuclear antigen EB
38	17	77.3	28	1	LFECL	hypothetical prote
39	17	77.3	28	2	G90638	C-type natriuretic
40	17	77.3	28	2	G85489	leu operon leader
41	16	72.7	16	2	151879	cystathionine beta
42	16	72.7	23	2	A36399	leu operon leader
43	16	72.7	23	2	S43469	heterodisulfide re
44	16	72.7	24	2	S29749	serum albumin - do
45	16	72.7	29	2	S78326	conserved hypothet
```

ALIGNMENTS

RESULT 1
SPPGNK
neuromedin K - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004
C;Accession: A01560
R;Kangawa, K.; Minamino, N.; Fukuda, A.; Matsuo, H.
Biochem. Biophys. Res. Commun. 114, 533-540, 1983
A;Title: Neuromedin K; a novel mammalian tachykinin identified in porcine spinal cord.
A;Reference number: A01560; MUID:83282812; PMID:6576785
A;Accession: A01560
A;Molecule type: protein
A;Residues: 1-10 <KAN>
A;Cross-references: UNIPROT:P01292; UNIPARC:UPI000003312EA
A;Note: the structure of the peptide was confirmed by synthesis
C;Comment: The biological source of this peptide is spinal cord. It stimulates smooth mus
C;Superfamily: neurokinin B precursor
C;Keywords: amidated carboxyl end; hormone; spinal cord
F;10/Modified site: amidated carboxyl end (Met) #status experimental

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Query Match             90.9%;  Score 20; DB 1; Length 10;
Best Local Similarity   80.0%;  Pred. No. 20;
       Matches    4;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy           1  FXGLM 5
                 | | |
Db           6  FVGLM 10
```

RESULT 2
JN0024
neurokinin A - chicken
C;Species: Gallus gallus (chicken)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JN0024
R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
Regul. Pept. 20, 171-180, 1988
A;Title: [Arg3]substance P and neurokinin A from chicken small intestine.
A;Reference number: JN0023; MUID:8820 4263; PMID:2452461
A;Accession: JN0024
A;Molecule type: protein
A;Residues: 1-10 <CON>
A;Cross-references: UNIPROT:P19851; UNIPARC:UPI0000003521C
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;10/Modified site: amidated carboxyl end (Met) #status predicted

```
Query Match             90.9%;  Score 20; DB 2; Length 10;
Best Local Similarity   80.0%;  Pred. No. 20;
       Matches    4;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy           1  FXGLM 5
```

Db 6 FVGLM 10
         |||

RESULT 3
B49581
sialokinin II - yellow fever mosquito
A;Species: Aedes aegypti (yellow fever mosquito)
A;Molecule type: protein
A;Status: preliminary
A;Reference number: B49581
A;Accession: B49581
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
A;Cross-references: UNIPARC:UPI000001336FEC
A;Residues: 1-10 <CHA>
A;Experimental source: Rockefeller; salivary gland
A;Title: Sialokinin I and II; vasodilatory tachykinins from the yellow fever mosquito Ae
R;Champagne, D.E.; Ribeiro, J.M.
Proc. Natl. Acad. Sci. U.S.A. 91, 138-142, 1994
C;Accession: B49581
A;Reference number: A49581; MUID:94105119; PMID:8278354
A;Note: sequence extracted from NCBI backbone (NCBIP:141842)

Query Match   90.9%; Score 20; DB 2; Length 10;
Best Local Similarity 80.0%;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FXGLM 5
         |||
Db 6 FVGLM 10

RESULT 4
S23307
neurokinin A - rainbow trout
A;Species: Oncorhynchus mykiss (rainbow trout)
A;Molecule type: protein
A;Status: preliminary
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
A;Accession: S23307
R;Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the coo
A;Reference number: S23186; MUID:92298992; PMID:1376687
A;Accession: S23307
A;Residues: 1-10 <JEN>
A;Cross-references: UNIPROT:P28500; UNIPARC:UPI000003521D

Query Match   90.9%; Score 20; DB 2; Length 10;
Best Local Similarity 80.0%;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FXGLM 5
         |||
Db 6 FVGLM 10

RESULT 5
S23186
neurokinin A - Atlantic cod
A;Species: Gadus morhua (Atlantic cod)
A;Molecule type: protein
A;Status: preliminary
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
A;Accession: S23186
R;Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod
A;Reference number: S23186; MUID:92298992; PMID:1376687
A;Accession: S23186
A;Residues: 1-10 <JEN>
A;Cross-references: UNIPROT:P28500; UNIPARC:UPI000003521D

A;Note: neurokinin A is derived by post-translational processing of preprotachykinin A
C;Keywords: neuropeptide; amidated carboxyl end; tachykinin
F;10/Modified site: amidated carboxyl end (Met) #status predicted

Query Match   90.9%; Score 20; DB 2; Length 10;
Best Local Similarity 80.0%;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FXGLM 5
         |||
Db 6 FVGLM 10

RESULT 6
S07202
phyllomedusin - two-colored leaf frog
A;Species: Phyllomedusa bicolor (two-colored leaf frog)
C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 16-Aug-2004
A;Accession: S07202
R;Anastasi, A.; Falconieri Erspamer, G.
Experientia 26, 866-967, 1970
A;Title: Occurrence of phyllomedusin, a physalaemin-like decapeptide, in the skin of Phy
A;Reference number: S07202; MUID:70267748; PMID:5452018
A;Accession: S07202
A;Molecule type: protein
A;Residues: 1-10 <ANA>
A;Cross-references: UNIPROT:P08610; UNIPARC:UPI000001336FE5
F;/Modified site: amidated carboxyl end; pyroglutamic acid
F;/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match   90.9%; Score 20; DB 2; Length 10;
Best Local Similarity 80.0%;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FXGLM 5
         |||
Db 6 FIGLM 10

RESULT 7
C61033
ranatachykinin C - bullfrog
A;Species: Rana catesbeiana (bullfrog)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Aug-2004
A;Accession: C61033; JE0428
R;Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.
Regul. Pept. 42(Suppl.1), S12, 1992
A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and inte
A;Reference number: A61033
A;Accession: C61033
A;Molecule type: protein
A;Residues: 1-10 <KAN>
A;Cross-references: UNIPROT:P22690; UNIPARC:UPI000001336FDF
A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and inte
R;Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 177, 588-595, 1991
A;Reference number: JE0428
A;Cross-references: UNIPROT:P22690; UNIPARC:UPI000001336FDF
A;Accession: JE0428; MUID:91254337; PMID:2043143
A;Residues: 1-10 <KOZ>
A;Cross-references: UNIPARC:UPI000001336FDF
C;Keywords: amidated carboxyl end; neuropeptide
F;10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match   90.9%; Score 20; DB 2; Length 10;
Best Local Similarity 80.0%;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FXGLM 5
         |||
Db 6 FIGLM 10

A;Molecule type: protein
A;Accession: S23186
A;Residues: 1-10 <JEN>
A;Cross-references: UNIPROT:P28500; UNIPARC:UPI000003521D
A;Experimental source: brain
C;Function:
A;Description: may play a physiological role in the regulation of cardiovascular and gas

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: November 26, 2005, 03:17:04 ; Search time 122.5 Seconds
(without alignments)
28.797 Million cell updates/sec

Title: US-10-805-881-4
Perfect score: 22
Sequence: 1 FXGLM 5

Scoring table: BLOSUM62
Searched: Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 2166443 seqs, 705528306 residues

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length DB	Match DB	ID	Description
1	21	95.5	13	1	CP1_APLCA	Q10998 aplysia cal
2	20	90.9	10	1	TKN1_SCYCA	P08608 scyliorhinu
3	20	90.9	10	1	TKNB_CHICK	P19851 gallus gall
4	20	90.9	10	1	TKNB_GADMO	P69144 gadus morhu
5	20	90.9	10	1	TKNB_ONCMY	P69143 oncorhynchu
6	20	90.9	10	1	TKNB_RANCA	P22689 rana catesb
7	20	90.9	10	1	TKNB_RANRI	P22689 rana ridibu
8	20	90.9	10	1	TKNC_RANCA	P22690 rana catesb
9	20	90.9	10	1	TKN_PIG	P67934 sus scrofa
10	20	90.9	10	1	TKNK_RANRI	P67935 rana ridibu
11	20	90.9	10	1	TKN_PHYBI	P08610 phyllomedus
12	20	90.9	10	1	TKS1_AEDAE	P42634 aedes aegyp
13	20	90.9	10	1	TKS2_AEDAE	P42635 aedes aegyp
14	20	90.9	10	1	TKN1_PSEGU	P42986 pseudophryn
15	20	90.9	11	1	TKN1_UPEIN	P82026 uperoleia i
16	20	90.9	11	1	TKN1_UPERU	P08612 uperoleia r
17	20	90.9	11	1	TKN2_PSEGU	P42987 pseudophryn
18	20	90.9	11	1	TKN2_UPERU	P08616 uperoleia r
19	20	90.9	11	1	TKN3_PSEGU	P42988 pseudophryn
20	20	90.9	11	1	TKN4_PSEGU	P42989 pseudophryn
21	20	90.9	11	1	TKN5_PSEGU	P42990 pseudophryn
22	20	90.9	11	1	TKNA_CAVPO	P67932 cavia porce
23	20	90.9	11	1	TKNA_CHICK	P19850 gallus gall
24	20	90.9	11	1	TKNA_GADMO	P28498 gadus morhu
25	20	90.9	11	1	TKNA_HORSE	P67933 equus cabal
26	20	90.9	11	1	TKNA_ONCMY	P28499 oncorhynchu
27	20	90.9	11	1	TKNA_RANCA	P22688 rana catesb
28	20	90.9	11	1	TKNA_RANRI	P29207 rana ridibu
29	20	90.9	11	1	TKNA_SCYCA	P41333 scyliorhinu
30	20	90.9	11	1	TKN_ELECI	P62933 eledone cir
31	20	90.9	11	1	TKN_ELEMO	P62934 eledone mos
32	20	90.9	11	1	TKN_PHYFU	P08615 physalaemus
33	20	90.9	11	2	Q9UAR8_AEDAE	Q9uar8 aedes aegyp
34	20	90.9	12	1	TKN1_KASMA	P08613 kassina mac
35	20	90.9	12	1	TKN_KASSE	P08611 kassina sen
36	20	90.9	14	1	TKNM_RANMA	P40951 rana margar
37	20	90.9	16	1	TKN1_TORMA	Q71248 torpedo mar
38	20	90.9	18	1	TKN2_SCYCA	P08609 scyliorhinu
39	20	90.9	20	1	TKNC_CARAU	P25421 carassius a
40	20	90.9	20	2	Q9PRZ3_ONCMY	oncorhynchu
41	20	90.9	21	2	Q9PS31_ALLMI	alligator m
42	20	90.9	24	2	Q9PRP3_SPHLE	sphyrna lew
43	20	86.4	29	2	Q673E3_9CHLR	dehalococco
44	20	86.4	27	2	Q9XAV0_PORGI	porphyromon
45	18	81.8	12	1	TKN2_KASMA	P08614 kassina mac

ALIGNMENTS

RESULT 1
CP1_APLCA

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ID   CP1_APLCA      STANDARD;      PRT;    13 AA.
AC   Q10998;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Cerebral peptide 1 (CP1).
OS   Aplysia californica (California sea hare).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC   Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
OC   Aplysioidea; Aplysiidae; Aplysia.
OX   NCBI_TaxID=6500;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Ganglion;
RX   MEDLINE=97001771; PubMed=8844763;
RA   Phares G.A., Lloyd P.E.;
RT   "Purification, primary structure, and neuronal localization of
RT   cerebral peptide 1 from Aplysia.";
RL   Peptides 17:753-761(1996).
CC   -!- FUNCTION: May function as a peptide transmitter.
CC   -!- TISSUE SPECIFICITY: Found predominantly in the cerebral and pedal
CC       ganglia.
CC   -----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
KW   Direct protein sequencing.
SQ   SEQUENCE   13 AA;  1314 MW;  9DBC3CE82C667B05 CRC64;
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Query Match   95.5%; Score 21; DB 1; Length 13;
Best Local Similarity   80.0%;
Matches   4; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Qy          1 FXGLM 5
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Db          1 FSGLM 5
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RESULT 2
TKN1_SCYCA

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ID   TKN1_SCYCA     STANDARD;      PRT;    10 AA.
AC   P08608;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Scyliorhinin-1 (Scyliorhinin I).
OS   Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
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OC   Scyliorhinidae; Scyliorhinus.
OX   NCBI_TaxID=7830;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Intestine;
RX   MEDLINE=8619829; PubMed=2422058; DOI=10.1016/0014-5793(86)80521-X;
RA   Conlon J.M., Deacon C.F., O'Toole L., Thim L.;
RT   "Scyliorhinin I and II: two novel tachykinins from dogfish gut.";
RL   FEBS Lett. 200:111-116(1986).
RN   [2]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=9292508; PubMed=7685693;
RA   Waugh D., Wang Y., Hazon N., Balment R.J., Conlon J.M.;
RT   "Primary structures and biological activities of substance-P-related
RT   peptides from the brain of the dogfish, Scyliorhinus canicula.";
RL   Eur. J. Biochem. 214:469-474(1993).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC   evoke behavioral responses, are potent vasodilators and
CC   secretagogues, and contract (directly or indirectly) many smooth
CC   muscles.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
CC
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC
DR   PIR; A24867; A24867.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Amidation; Direct protein sequencing; Neuropeptide; Tachykinin.
FT   MOD_RES   10   10   Methionine amide.
SQ   SEQUENCE   10 AA;   1219 MW; D0602D6B59C33AA9 CRC64;

Qy   1 FXGLM 5
              |||||
Db   6 FXGLM 10

Query Match   Best Local Similarity   90.9%; Score 20; DB 1; Length 10;
                        Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Pred. No. 2e+02;

RESULT 3
ID   TKNB_CHICK   STANDARD;   PRT;   10 AA.
AC   P19851;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Neurokinin A (Substance K) (Neuromedin L).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Intestine;
RX   MEDLINE=88204263; PubMed=2452461; DOI=10.1016/0167-0115(88)90050-X;
RA   Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
RT   "[Arg3]substance P and neurokinin A from chicken small intestine.";
RL   Regul. Pept. 20:171-180(1988).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC   evoke behavioral responses, are potent vasodilators and
CC   secretagogues, and contract (directly or indirectly) many smooth
CC   muscles.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
CC
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC
DR   PIR; JN0024; JN0024.
DR   PDB; 1N6T; NMR; A=1-10.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   Pfam; PF02202; TACHYKININ; 1.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   3D-structure; Amidation; Direct protein sequencing; Neuropeptide;
KW   Tachykinin.
FT   MOD_RES   10   10   Methionine amide.
SQ   SEQUENCE   10 AA;   1134 MW; 8A6B4062C9D5BAB1 CRC64;

Qy   1 FXGLM 5
              |||||
Db   6 FXGLM 10

Query Match   Best Local Similarity   90.9%; Score 20; DB 1; Length 10;
                        Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Pred. No. 2e+02;

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ID   TKNB_GADMO   STANDARD;   PRT;   10 AA.
AC   P69144; P28500;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Neurokinin A (Substance K) (Neuromedin L).
OS   Gadus morhua (Atlantic cod).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
OX   NCBI_TaxID=8049;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=92298992; PubMed=1376687;
RA   Jensen J., Conlon J.M.;
RT   "Substance-P-related and neurokinin-A-related peptides from the brain
RT   of the cod and trout.";
RL   Eur. J. Biochem. 206:659-664(1992).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC   evoke behavioral responses, are potent vasodilators and
CC   secretagogues, and contract (directly or indirectly) many smooth
CC   muscles.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
CC
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC
DR   PIR; S23186; S23186.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   Pfam; PF02202; TACHYKININ; 1.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Amidation; Direct protein sequencing; Neuropeptide; Tachykinin.
FT   MOD_RES   10   10   Methionine amide (By similarity).
SQ   SEQUENCE   10 AA;   1145 MW; 136B4062C9D5B440 CRC64;

Qy   1 FXGLM 5
              |||||
Db   6 FXGLM 10

Query Match   Best Local Similarity   90.9%; Score 20; DB 1; Length 10;
                        Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Pred. No. 2e+02;

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                                 GenCore version 5.1.6

                                 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:           November 26, 2005, 03:06:43 ; Search time 20 Seconds
                                               (without alignments)
                                               20.669 Million cell updates/sec

Title:            US-10-805-881-4
Perfect score:    22
Sequence:         1 FXGLM 5
Scoring table:    BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:         572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:        265581

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Issued Patents AA:*
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                  4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                  6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                      SUMMARIES

                   %
Result            Query
No.    Score  Match  Length DB  ID                Description
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 1      20    90.9      5   1   US-07-753-909B-3  Sequence 3, Appli
 2      20    90.9      5   1   US-07-934-553-2   Sequence 2, Appli
 3      20    90.9      5   1   US-08-269-288-1   Sequence 1, Appli
 4      20    90.9      5   1   US-08-225-474-2   Sequence 2, Appli
 5      20    90.9      5   1   US-08-391-910-1   Sequence 1, Appli
 6      20    90.9      5   1   US-08-418-994-1   Sequence 1, Appli
 7      20    90.9      5   1   US-08-391-814-1   Sequence 1, Appli
 8      20    90.9      5   1   US-08-441-591-61  Sequence 61, Appl
 9      20    90.9      5   1   US-08-303-362A-61 Sequence 61, Appl
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14      20    90.9      5   6   US-07-737-371E-6  Sequence 6, Appli
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16      20    90.9      5   1   US-09-265-690C-1  Sequence 1, Appli
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24      20    90.9      5   1   US-10-134-187-3   Sequence 3, Appli
25      20    90.9      5   2   US-09-657-276-604 Sequence 604, App
26      20    90.9      5   4   PCT-US95-05600-78 Sequence 78, Appl
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31      20    90.9      6   1   US-07-737-371E-52 Sequence 52, Appli
32      20    90.9      6   1   US-09-317-125-5   Sequence 5, Appli
33      20    90.9      6   2   US-09-428-692-39  Sequence 39, Appl
34      20    90.9      6   2   US-09-428-692-41  Sequence 41, Appl
35      20    90.9      6   2   US-09-623-548A-595 Sequence 595, App
36      20    90.9      6   2   US-09-623-548A-597 Sequence 597, App
37      20    90.9      6   2   US-09-623-548A-601 Sequence 601, App
38      20    90.9      6   2   US-09-657-276-595 Sequence 595, App
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41      20    90.9      6   1   US-07-712-828B-7  Sequence 7, Appli
42      20    90.9      7   1   US-07-737-371E-8  Sequence 8, Appli
43      20    90.9      7   1   US-07-737-371E-51 Sequence 51, Appli
44      20    90.9      7   2   US-09-428-692-42  Sequence 42, Appl
45      20    90.9      7   2   US-09-623-548A-530 Sequence 530, App
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                                     ALIGNMENTS

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RESULT 1
US-07-753-909B-3
; Sequence 3, Application US/07753909B
; Patent No. 5304632
; GENERAL INFORMATION:
;     APPLICANT: Vaudry, Hubert
;     APPLICANT: Conlon, Michael J.
;     TITLE OF INVENTION: Neuropeptides of the Tachykinin Family
;     NUMBER OF SEQUENCES: 3
;     CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Zarley, McKee, Thomte, Voorhees, and Sease
;     STREET: 801 Grand, Suite 3200
;     CITY: Des Moines
;     STATE: Iowa
;     COUNTRY: United States
;     ZIP: 50309
; COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/07/753,909B
; FILING DATE: 19910903
;     CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: FR 9106759
;     FILING DATE: 04-JUN-1991
; ATTORNEY/AGENT INFORMATION:
;     NAME: Sease, Edmund J.
;     REGISTRATION NUMBER: 24,741
; TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (515)-288-3667
;     TELEFAX: (515)-288-1338
; INFORMATION FOR SEQ ID NO: 3:
;     SEQUENCE CHARACTERISTICS:
;     LENGTH: 5 amino acids
;     TYPE: AMINO ACID
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     FRAGMENT TYPE: C-terminal
;     ORIGINAL SOURCE:
;     ORGANISM: Rana ridibunda
;     DEVELOPMENTAL STAGE: adult
;     TISSUE TYPE: brain
US-07-753-909B-3

Query Match             90.9%;  Score 20;  DB 1;  Length 5;
Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
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Qy   1 FXGLM 5
          |||||
Db   1 FXGLM 5

Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 2
US-07-934-553-2
; Sequence 2, Application US/0793453
; Patent No. 5314690
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, ROY
; APPLICANT: HARRIS, KATHLEEN E
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IgE
; TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TILTON, FALLON, LUNGMUS & CHESTNUT
; STREET: 100 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,553
; FILING DATE: 19920821
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/705,071
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTRESS, SUSAN B
; REGISTRATION NUMBER: 31,327
; REFERENCE/DOCKET NUMBER: NU-9033CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/456-8000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-07-934-553-2

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Db   1 FFGLM 5

Query Match   90.9%; Score 20; DB 1; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches   4; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

RESULT 3
US-08-269-288-1
; Sequence 1, Application US/08269288
; Patent No. 5491140
; GENERAL INFORMATION:
; APPLICANT: Bruns, Robert F.
; APPLICANT: Gehlert, Donald R.
; APPLICANT: Howbert, James J.
; APPLICANT: Lunn, William H.W.
; TITLE OF INVENTION: NAPHTHYL TACHYKININ RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company

; STREET: Lilly Corporate Center/1104
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/269,288
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9715
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-269-288-1

Qy   1 FXGLM 5
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Db   1 FXGLM 5

Query Match   90.9%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 4
US-08-225-474-2
; Sequence 2, Application US/08225474
; Patent No. 5560915
; GENERAL INFORMATION:
; APPLICANT: Patterson, Roy
; APPLICANT: Harris, Kathleen E.
; TITLE OF INVENTION: Method and Composition for Treating
; TITLE OF INVENTION: IgE Mediated Allergies
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
; STREET: 100 S. Wacker Drive, Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,474
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,553
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/705,071
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tilton, Timothy L.

OM protein - protein search, using sw model

Copyright (c) 1993 - 2005 Compugen Ltd.　　　GenCore version 5.1.6

Run on: November 26, 2005, 03:13:24 ; Search time 57.5 Seconds
　　　　　　　　　　　　　　　　　　　　　　(without alignments)
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Perfect Score: 22
Sequence: 1 FXGLM 5
Scoring table: BLOSUM62
Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters:　　　439079

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
　　　　　　　　　Maximum Match 100%
　　　　　　　　　Listing first 45 summaries

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　　2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
　　3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
　　4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
　　5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
　　6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	95.5	12	4	US-10-172-425B-16	Sequence 16, Appl
2	21	95.5	15	5	US-10-525-113-10	Sequence 10, Appl
3	21	95.5	15	5	US-10-525-113-11	Sequence 11, Appl
4	21	95.5	15	5	US-10-525-113-12	Sequence 12, Appl
5	21	95.5	15	4	US-10-525-113-13	Sequence 13, Appl
6	21	95.5	4	5	US-10-172-425B-17	Sequence 17, Appl
7	21	95.5	21	4	US-10-172-425B-2	Sequence 2, Appl
8	21	95.5	29	3	US-09-864-761-34512	Sequence 34512, A
9	20	90.9	5	3	US-09-265-690C-1	Sequence 1, Appl
10	20	90.9	5	4	US-09-265-690C-4	Sequence 4, Appl
11	20	90.9	5	3	US-10-230-133-4	Sequence 4, Appl
12	20	90.9	5	4	US-10-053-669-1	Sequence 1, Appl
13	20	90.9	5	4	US-10-053-669-4	Sequence 4, Appl
14	20	90.9	5	4	US-10-134-187-3	Sequence 3, Appl
15	20	90.9	5	4	US-10-688-741-3	Sequence 3, Appl
16	20	90.9	5	4	US-10-695-536-4	Sequence 4, Appl
17	20	90.9	5	4	US-10-805-881-1	Sequence 1, Appl
18	20	90.9	5	4	US-10-805-881-4	Sequence 4, Appl
19	20	90.9	5	4	US-10-720-039-3	Sequence 3, Appl
20	20	90.9	5	5	US-10-497-628-15	Sequence 15, Appl
21	20	90.9	5	6	US-11-018-590-4	Sequence 4, Appl
22	20	90.9	5	6	US-11-066-697-604	Sequence 604, App
23	20	90.9	5	6	US-11-066-697-604	Sequence 604, App
24	20	90.9	4	5	US-11-025-494-3	Sequence 3, Appli
25	20	90.9	6	4	US-10-168-789A-38	Sequence 38, Appl
26	20	90.9	6	5	US-10-497-628-14	Sequence 14, Appl
27	20	90.9	6	6	US-11-066-697-595	Sequence 595, App
28	20	90.9	6	6	US-11-066-697-597	Sequence 597, App
29	20	90.9	6	6	US-11-066-697-601	Sequence 601, App
30	20	90.9	6	4	US-10-036-542-110	Sequence 110, App
31	20	90.9	6	4	US-10-036-542-111	Sequence 111, App
32	20	90.9	6	4	US-10-168-789A-37	Sequence 37, Appl
33	20	90.9	7	4	US-10-168-789A-36	Sequence 2, Appli
34	20	90.9	7	4	US-09-910-552-36	Sequence 2, Appli
35	20	90.9	7	5	US-10-720-039-2	Sequence 2, Appli
36	20	90.9	7	5	US-10-688-741-2	Sequence 2, Appli
37	20	90.9	7	5	US-11-066-697-530	Sequence 530, App
38	20	90.9	7	6	US-11-066-697-596	Sequence 596, App
39	20	90.9	7	6	US-11-066-697-607	Sequence 607, App
40	20	90.9	8	3	US-10-134-187-2	Sequence 2, Appli
41	20	90.9	8	4	US-09-910-552-36	Sequence 36, Appl
42	20	90.9	8	4	US-10-643-465-36	Sequence 36, Appl
43	20	90.9	8	5	US-10-497-628-12	Sequence 12, Appl
44	20	90.9	5	5	US-10-168-789A-36	Sequence 36, Appl
45	20	90.9	6	6	US-11-066-697-583	Sequence 583, App

ALIGNMENTS

RESULT 1
US-10-172-425B-16
; Sequence 16, Application US/10172425B
; Publication No. US2003014790BA1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
; TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
; FILE REFERENCE: A31967-PCT-USA-A-A 066031.0164
; CURRENT APPLICATION NUMBER: US/10/172,425B
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 09/150,947
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-172-425B-16

Query Match　　　　95.5%; Score 21; DB 4; Length 12;
Best Local Similarity　 80.0%; Pred. No. 1e+02; Length 12;
Matches　　4; Conservative　0; Mismatches　1; Indels 0; Gaps 0;

Qy　　1 FXGLM 5
　　　　　　|||
Db　　5 FTGLM 9

RESULT 2
US-10-525-113-10
; Sequence 10, Application US/10525113
; Publication No. US2005024009A1
; GENERAL INFORMATION:
; APPLICANT: MERCK PATENT GMBH
; APPLICANT: CARR, Francis J.
; APPLICANT: BAKER, Matthew
; APPLICANT: CARTER, Graham
; TITLE OF INVENTION: T-CELL EPITOPES IN STAPHYLOCOCCAL
; TITLE OF INVENTION: ENTEROTOXIN B
; FILE REFERENCE: MER-138
; CURRENT APPLICATION NUMBER: US/10/525,113
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: PCT/EP2003/009116

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;  PRIOR FILING DATE: 2003-08-18
;  PRIOR APPLICATION NUMBER: EP 02018229.1
;  PRIOR FILING DATE: 2002-08-21
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 10
;  TYPE: PRT
;  LENGTH: 15
;  ORGANISM: Staphylococcus aureus
US-10-525-113-10

  Query Match  95.5%;  Score 21;  DB 5;  Length 15;
  Best Local Similarity  80.0%;  Pred. No. 1.3e+02;
  Matches   4;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy   1 FXGLM 5
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Db  11 FTGLM 15


RESULT 3
US-10-525-113-11
;  Sequence 11, Application US/10525113
;  Publication No. US20050240009A1
;  GENERAL INFORMATION:
;  APPLICANT: MERCK PATENT GMBH
;  APPLICANT: CARR, Francis J.
;  APPLICANT: BAKER, Matthew
;  APPLICANT: CARTER, Graham
;  TITLE OF INVENTION: T-CELL EPITOPES IN STAPHYLOCOCCAL
;  FILE REFERENCE: MER-138
;  CURRENT APPLICATION NUMBER: US/10/525,113
;  CURRENT FILING DATE: 2005-02-18
;  PRIOR APPLICATION NUMBER: PCT/EP2003/009116
;  PRIOR FILING DATE: 2003-08-18
;  PRIOR APPLICATION NUMBER: EP 02018229.1
;  PRIOR FILING DATE: 2002-08-21
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 11
;  LENGTH: 15
;  TYPE: PRT
;  ORGANISM: Staphylococcus aureus

  Query Match  95.5%;  Score 21;  DB 5;  Length 15;
  Best Local Similarity  80.0%;  Pred. No. 1.3e+02;
  Matches   4;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy   1 FXGLM 5
        ||||
Db   5 FTGLM 9


RESULT 4
US-10-525-113-12
;  Sequence 12, Application US/10525113
;  Publication No. US20050240009A1
;  GENERAL INFORMATION:
;  APPLICANT: MERCK PATENT GMBH
;  APPLICANT: CARR, Francis J.
;  APPLICANT: BAKER, Matthew
;  APPLICANT: CARTER, Graham
;  TITLE OF INVENTION: T-CELL EPITOPES IN STAPHYLOCOCCAL
;  FILE REFERENCE: MER-138
;  CURRENT APPLICATION NUMBER: US/10/525,113
;  CURRENT FILING DATE: 2005-02-18
;  PRIOR APPLICATION NUMBER: PCT/EP2003/009116
;  PRIOR FILING DATE: 2003-08-18
;  PRIOR APPLICATION NUMBER: EP 02018229.1
;  PRIOR FILING DATE: 2002-08-21

Qy   1 FXGLM 5
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Db   8 FTGLM 12
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RESULT 5
US-10-525-113-13
;  Sequence 13, Application US/10525113
;  Publication No. US20050240009A1
;  GENERAL INFORMATION:
;  APPLICANT: MERCK PATENT GMBH
;  APPLICANT: CARR, Francis J.
;  APPLICANT: BAKER, Matthew
;  APPLICANT: CARTER, Graham
;  TITLE OF INVENTION: T-CELL EPITOPES IN STAPHYLOCOCCAL
;  FILE REFERENCE: MER-138
;  CURRENT APPLICATION NUMBER: US/10/525,113
;  CURRENT FILING DATE: 2005-02-18
;  PRIOR APPLICATION NUMBER: PCT/EP2003/009116
;  PRIOR FILING DATE: 2003-08-18
;  PRIOR APPLICATION NUMBER: EP 02018229.1
;  PRIOR FILING DATE: 2002-08-21
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 13
;  LENGTH: 15
;  TYPE: PRT
;  ORGANISM: Staphylococcus aureus

  Query Match  95.5%;  Score 21;  DB 5;  Length 15;
  Best Local Similarity  80.0%;  Pred. No. 1.3e+02;
  Matches   4;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy   1 FXGLM 5
        ||||
Db   5 FTGLM 9


RESULT 6
US-10-172-425B-17
;  Sequence 17, Application US/10172425B
;  Publication No. US20030147908A1
;  GENERAL INFORMATION:
;  APPLICANT: Kaempfer, Raymond
;  APPLICANT: Arad, Gila
;  TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
;  TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
;  FILE REFERENCE: A31967-PCT-USA-A-A 066031.0164
;  CURRENT APPLICATION NUMBER: US/10/172,425B
;  CURRENT FILING DATE: 2002-06-13
;  PRIOR APPLICATION NUMBER: 09/150,947
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: PCT/IL97/00438
;  PRIOR FILING DATE: 1997-12-30
;  PRIOR APPLICATION NUMBER: ISRAEL 119938
;  PRIOR FILING DATE: 1996-12-30
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 17

  Query Match  95.5%;  Score 21;  DB 5;  Length 15;
  Best Local Similarity  80.0%;  Pred. No. 1.3e+02;
  Matches   4;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy   1 FXGLM 5
        ||||
Db   2 FTGLM 6
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OM protein - protein search, using sw model

Run on: November 26, 2005, 03:09:53 ; Search time 3.57143 Seconds
(without alignments)
4.243 Million cell updates/sec

Title: US-10-805-881-4
Perfect score: 22
Sequence: 1 FXGLM 5
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 17545 seqs, 3030971 residues
Total number of hits satisfying chosen parameters: 7285

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16	72.7	28	7	US-11-021-441-50	Sequence 50, Appl
2	15	68.2	8	7	US-11-054-515-3132	Sequence 3132, Ap
3	15	68.2	12	1	US-10-923-605-4	Sequence 4, Appli
4	15	68.2	13	1	US-10-934-818-4	Sequence 4, Appli
5	15	68.2	13	1	US-10-511-559-478	Sequence 478, App
6	15	68.2	13	1	US-10-511-559-479	Sequence 479, App
7	15	68.2	13	1	US-10-511-559-480	Sequence 480, App
8	15	68.2	13	1	US-10-511-559-481	Sequence 481, App
9	15	68.2	13	1	US-10-511-559-482	Sequence 482, App
10	15	68.2	16	7	US-11-054-515-2157	Sequence 2157, Ap
11	15	68.2	19	1	US-10-503-575-149	Sequence 149, App
12	15	68.2	19	1	US-10-503-575-161	Sequence 161, App
13	15	68.2	24	1	US-10-989-226-31	Sequence 31, Appl
14	15	68.2	30	1	US-10-986-501-177	Sequence 177, App
15	14	63.6	20	7	US-11-022-562-147	Sequence 147, App
16	14	63.6	21	1	US-10-939-890-523	Sequence 523, App
17	14	63.6	21	1	US-10-939-890-551	Sequence 551, App
18	14	63.6	21	1	US-10-939-890-552	Sequence 552, App
19	14	63.6	8	1	US-10-939-890-576	Sequence 576, App
20	13	59.1	7	7	US-11-054-515-3098	Sequence 3098, Ap
21	13	59.1	10	1	US-10-614-599-45	Sequence 45, Appl
22	13	59.1	11	1	US-10-614-599-47	Sequence 47, Appl
23	13	59.1	11	7	US-11-016-706-49	Sequence 49, Appl
24	13	59.1	12	7	US-11-054-515-2884	Sequence 2884, Ap
25	13	59.1	14	7	US-11-054-515-2374	Sequence 2374, Ap
26	13	59.1	17	1	US-10-723-207-63	Sequence 63, Appl
27	13	59.1	17	7	US-11-054-515-3025	Sequence 3025, Ap
28	13	59.1	18	7	US-11-054-515-2752	Sequence 2752, Ap
29	13	59.1	18	7	US-11-054-515-2802	Sequence 2802, Ap
30	13	59.1	18	7	US-11-054-515-2880	Sequence 2880, Ap
31	13	59.1	18	7	US-11-054-515-2917	Sequence 2917, Ap
32	13	59.1	20	7	US-11-022-562-175	Sequence 175, App
33	13	59.1	20	7	US-11-054-515-2131	Sequence 2131, Ap
34	13	59.1	21	1	US-10-939-890-597	Sequence 597, App
35	12	54.5	9	1	US-10-516-768-35	Sequence 35, Appl
36	12	54.5	9	7	US-11-032-498-7	Sequence 7, Appl
37	12	54.5	9	7	US-11-032-498-17	Sequence 17, Appl
38	12	54.5	10	7	US-11-054-515-3200	Sequence 3200, Ap
39	12	54.5	11	7	US-11-057-708-25	Sequence 25, Appl
40	12	54.5	11	1	US-10-502-145-34	Sequence 34, Appl
41	12	54.5	13	1	US-10-939-890-192	Sequence 192, App
42	12	54.5	13	1	US-10-939-890-194	Sequence 194, App
43	12	54.5	13	1	US-10-511-559-113	Sequence 113, App
44	12	54.5	13	1	US-10-511-559-114	Sequence 114, App
45	12	54.5	13	1	US-10-511-559-115	Sequence 115, App

ALIGNMENTS

RESULT 1
US-11-021-441-50
; Sequence 50, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 28217003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/599,377
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/23881
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/883,599
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/615,287
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06
; SOFTWARE: FastSEQ for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 50
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-11-021-441-50

Query Match 72.7%; Score 16; DB 7; Length 28;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy  1 FXGL 4
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Db 17 FSGL 20
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RESULT 2
US-11-054-515-3132
; Sequence 3132, Application US/11054515
; Publication No. US20050255532A1

GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3132
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3132

Query Match   68.2%; Score 15; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches   3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3 GLM 5
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Db   4 GLM 6

RESULT 3
US-10-923-605-4
; Sequence 4, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152700-00474US
; CURRENT APPLICATION NUMBER: US/10/923,605
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta33-42
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (2)
; OTHER INFORMATION: Xaa = amino hepatanoic acid
US-10-923-605-4

Query Match   68.2%; Score 15; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 18;
Matches   3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3 GLM 5
              |||
Db   3 GLM 5

RESULT 4
US-10-934-818-4
; Sequence 4, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152700-47200US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta33-42
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (2)
; OTHER INFORMATION: Xaa = amino hepatanoic acid
US-10-934-818-4

Query Match   68.2%; Score 15; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 18;
Matches   3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3 GLM 5
              |||
Db   3 GLM 5

RESULT 5
US-10-511-559-478
; Sequence 478, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 478
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension **.rup)** that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

   http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.